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(54) Title: NOVEL PROSTATE-SPECIFIC OR TESTIS-SPECIFIC NUCLEIC ACID MOLECULES, POLYPEPTIDES, AND DIAGNOSTIC AND THERAPEUTIC METHODS

(57) Abstract: The invention provides novel prostate-specific or testis-specific nucleic acid molecules, polypeptides, antibodies, and modulatory compounds for use in methods of diagnosing, treating, and preventing diseases and conditions of the prostate and testis, such as cancer.

5 NOVEL PROSTATE-SPECIFIC OR TESTIS-SPECIFIC
NUCLEIC ACID MOLECULES, POLYPEPTIDES, AND DIAGNOSTIC
AND THERAPEUTIC METHODS

Field of The Invention

10 The invention generally relates to the treatment of disorders associated with prostate and testis dysfunction and cell proliferation, and specifically relates to the identification and use of novel genes for diagnosis and treatment of such disorders.

15 Background of The Invention

Genitourinary disorders are often difficult to diagnose and treat effectively because they are present non-specifically. Two causes of genitourinary disorders are disorders of the prostate gland and the testis.

The prostate is a variable sized gland located in the male pelvis, and 20 is made up of several different cell types, including epithelial cells and stromal cells. Prostate-associated disorders include prostate cancer, benign prostatic hyperplasia, and prostatitis. The male hormone testosterone and other androgen related hormones have major roles in the growth and function of the prostate. The testis is also subject to many defects, 25 including developmental anomalies, inflammation, and cancer.

In men, prostate cancer is the most commonly diagnosed cancer and the second leading cause of cancer mortality following skin cancer. In the initial stages, prostate cancer is dependent on androgens for growth, and this dependence is the basis for androgen ablation therapy. In most cases, 30 however, prostate cancer progresses to an androgen-independent phenotype for which there is no effective therapy available at present.

Currently, there is limited information regarding the molecular details of prostate cancer progression. Several independent approaches resulted in the identification of a few highly prostate-enriched genes that may have unique roles in this process. The first such gene discovered was

5 Prostate Specific Antigen (PSA), the detection of which is currently used as a diagnostic tool and also as a marker for the progression of prostate cancer, albeit with significant limitations. More recently, several additional prostate-enriched genes were identified including prostate-specific membrane antigen (PSMA), prostate carcinoma tumor antigen 1 (PCTA-1),

10 NKX3.1, prostate stem cell antigen (PSCA), DD3, and PCGEM1.

It would be beneficial to provide reagents useful for the diagnosis and therapy of disorders associated with the prostate and the testis, as well as other tissues.

15 Summary of the Invention

The invention provides, in general, a novel prostate-specific or testis-specific nucleic acid molecules, polypeptides, antibodies, and modulatory compounds for use in methods of diagnosing, treating, and preventing diseases and conditions of the prostate and testis, such as cancer.

20 In a first aspect the invention provides a substantially pure prostate-specific or testis-specific polypeptide, including a sequence substantially identical to the sequence of any of SEQ ID NOS: 14, 29, 32, 34, 36, 41, or 53. In a preferred embodiment of the first aspect, the substantially pure prostate-specific or testis-specific polypeptide includes the sequence of any
25 of SEQ ID NOS: 14, 29, 32, 34, 36, 41, or 53. In another preferred embodiment, the invention provides an isolated nucleic acid molecule encoding a polypeptide of the first aspect, for example a nucleic acid

molecule including the sequence of any of SEQ ID NOS: 23, 28, 31, 33, 35, 40, or 52. Preferably, the polypeptide is derived from a mammal, e.g., a human.

In a second aspect, the invention provides an isolated prostate-specific or testis-specific nucleic acid molecule including a sequence substantially identical to SEQ ID NOS: 1-12, 22, 27, 30, and 51.

In a third aspect, the invention provides an isolated prostate-specific or testis-specific nucleic acid molecule consisting essentially of SEQ ID NOS: 15-21, 24-26, 42-50, and 54-70.

10 In preferred embodiments of some of the above aspects, the invention provides a vector, a cell, a cell including the vector, and a non-human transgenic animal including the isolated nucleic acid molecules.

15 In a fourth aspect, the invention provides an isolated nucleic acid molecule that hybridizes under high stringency conditions to the complement of any of the sequences set forth in SEQ ID NOS: 1-12, 15-28, 30, 31, 33, 35, 40, 42-50, 51, 52, or 54-70, where the isolated nucleic acid molecule encodes a prostate-specific or testis-specific polypeptide.

20 In a fifth aspect, the invention provides an isolated nucleic acid molecule, where the nucleic acid molecule includes a sequence that is antisense to the coding strand of any of the prostate-specific or testis-specific nucleic acid molecules set forth in SEQ ID NOS: 1-12, 15-28, 30, 31, 33, 35, 40, 42-50, 51, 52, or 54-70, or a fragment thereof.

25 In a sixth aspect, the invention provides a probe for analyzing a prostate-specific or testis-specific gene or homolog or fragment thereof, the probe having greater than 55% nucleotide sequence identity to a sequence encoding any of SEQ ID NOS: 1-12, 15-28, 30, 31, 33, 35, 40, 42-50, 51, 52, or 54-70, or fragment thereof, where the fragment includes at least six amino acids, and the probe hybridizes under high stringency conditions to at least a portion of a prostate-specific or testis-specific nucleic acid

molecule. In a preferred embodiment of this aspect, the probe has 100% complementarity to a nucleic acid molecule encoding any of SEQ ID NOS: 1-12, 15-28, 30, 31, 33, 35, 40, 42-50, 51, 52, or 54-70, or fragment thereof, where the fragment comprises at least six amino acids, and said probe

5 hybridizes under high stringency conditions to at least a portion of a prostate-specific or testis-specific nucleic acid molecule.

In a seventh aspect, the invention provides an antibody that specifically binds to a prostate-specific or testis-specific polypeptide that includes an amino acid sequence that is substantially identical to the amino

10 acid sequence of any of SEQ ID NOS: 14, 29, 32, 34, 36, 41, or 53.

In an eighth aspect, the invention provides a method of detecting a prostate-specific or testis-specific gene or fragment thereof in a cell, the method including contacting the nucleic acid molecule of any of SEQ ID NOS: 1-12, 15-28, 30, 31, 33, 35, 40, 42-50, 51, 52, or 54-70, or a fragment thereof, where the fragment is greater than about 18 nucleotides in length, with a preparation of genomic DNA from the cell, under high stringency hybridization conditions, and detecting DNA sequences having about 55% or greater nucleotide sequence identity to any of SEQ ID NOS: 1-12, 15-28, 30, 31, 33, 35, 40, 42-50, 51, 52, or 54-70, thus identifying a prostate-

15 specific or testis-specific gene or fragment thereof. Nucleotides encoding the polypeptides of SEQ ID NOS: 38, 39, or 71-73 can also be used in an embodiment of this aspect. In a preferred embodiment of this aspect, the method includes detecting a neoplastic or cancer cell in a patient predisposed to or at risk for cancer, for example, for prostate cancer.

20 In a ninth aspect, the invention provides a method for identifying a test compound that modulates the expression or activity of a prostate-specific or testis-specific polypeptide, the method including contacting the prostate-specific or testis-specific polypeptide with the test compound, and determining the effect of the test compound on the prostate-specific or

testis-specific polypeptide expression or activity. In a preferred embodiments of this aspect, the prostate-specific or testis-specific polypeptide includes an amino acid sequence substantially identical to the amino acid sequence of SEQ ID NOS: 14, 29, 32, 34, 36, 38, 39, 41, 53, or 5 71-73, and fragments and analogs thereof.

In a tenth aspect, the invention provides a method of treating a mammal having a disorder of the prostate or testis, the method including administering to the mammal a therapeutically effective amount of a compound that modulates the activity or expression of a prostate-specific or 10 testis-specific polypeptide, where the compound has a beneficial effect on the disorder in the mammal. In preferred embodiments of this aspect, the disorder is prostate cancer, the mammal is a human, or the prostate-specific or testis-specific polypeptide includes an amino acid sequence substantially identical to the amino acid sequence of SEQ ID NOS: 14, 29, 32, 34, 36, 15 38, 39, 41, 53, or 71-73, and fragments and analogs thereof.

In an eleventh aspect, the invention provides a pharmaceutical composition including at least one dose of a therapeutically effective amount of a prostate-specific or testis-specific polypeptide or fragment thereof, in a pharmaceutically acceptable carrier, the composition being 20 formulated for the treatment of a disorder of the prostate or testis.

In a twelfth aspect, the invention provides a kit for the analysis of a prostate-specific or testis-specific nucleic acid molecule, the kit including a nucleic acid molecule probe for analyzing a prostate-specific or testis-specific nucleic acid molecule present in a test subject.

25 In a thirteenth aspect, the invention provides a kit for the analysis of a prostate-specific or testis-specific polypeptide, the kit including an antibody for analyzing a prostate-specific or testis-specific polypeptide present in a test subject.

As used herein, by "polypeptide," "protein," or "polypeptide fragment" is meant a chain of two or more amino acids, regardless of any post-translational modification (e.g., glycosylation or phosphorylation), constituting all or part of a naturally or non-naturally occurring polypeptide. By "post-translational modification" is meant any change to a polypeptide or polypeptide fragment during or after synthesis. Post-translational modifications can be produced naturally (such as during synthesis within a cell) or generated artificially (such as by recombinant or chemical means). A protein can be made up of one or more polypeptides.

By "substantially pure polypeptide" or "substantially pure and isolated polypeptide" is meant a polypeptide (or a fragment thereof) that has been separated from components that naturally accompany it. Typically, the polypeptide is substantially pure when it is at least 60%, by weight, free from the proteins and naturally occurring organic molecules with which it is naturally associated. Preferably, the polypeptide is a prostate-specific or a testis-specific polypeptide that is at least 75%, more preferably at least 90%, and most preferably at least 99%, by weight, pure. A substantially pure prostate-specific or a testis-specific polypeptide may be obtained by standard techniques, for example, by extraction from a natural source (e.g., prostate or testis tissue or cell lines), by expression of a recombinant nucleic acid encoding a prostate-specific or a testis-specific polypeptide, or by chemically synthesizing the polypeptide. Purity can be measured by any appropriate method, e.g., by column chromatography, polyacrylamide gel electrophoresis, or HPLC analysis.

A protein or polypeptide is substantially free of naturally associated components when it is separated from those contaminants that accompany it in its natural state. Thus, a protein that is chemically synthesized or produced in a cellular system different from the cell from which it naturally originates will be substantially free from its naturally associated

components. Accordingly, substantially pure polypeptides not only include those derived from eukaryotic organisms but also those synthesized in *E. coli* or other prokaryotes.

The term "identity" is used herein to describe the relationship of the sequence of a particular nucleic acid molecule or polypeptide to the sequence of a reference molecule of the same type. For example, if a polypeptide or nucleic acid molecule has the same amino acid or nucleotide residue at a given position, compared to a reference molecule to which it is aligned, there is said to be "identity" at that position.

The level of sequence identity of a nucleic acid molecule or a polypeptide to a reference molecule is typically measured using sequence analysis software with the default parameters specified therein, such as the introduction of gaps to achieve an optimal alignment. The "identity" of two or more nucleic acid or polypeptide sequences can therefore be readily calculated by known methods, including but not limited to those described in *Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data*, Part I, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, and Devereux, eds., M. Stockton Press, New York, 1991; and Carillo and Lipman, SIAM J. Applied Math. 48:1073, 1988.

Methods to determine identity are available in publicly available computer programs. Computer program methods to determine identity between two sequences include, but are not limited to, the GCG program package (Devereux et al., Nucleic Acids Research 12(1): 387, 1984), BLASTP, BLASTN, and FASTA (Altschul et al., J. Mol. Biol. 215: 403 (1990). The well known Smith Waterman algorithm may also be used to

determine identity. The BLAST program is publicly available from NCBI and other sources (*BLAST Manual*, Altschul, et al., NCBI NLM NIH Bethesda, MD 20894). Searches can be performed in URLs such as the following <http://www.ncbi.nlm.nih.gov/BLAST/unfinishedgenome.html>; or

5 http://www.tigr.org/cgi-bin/BlastSearch/blast.cgi. These software programs match similar sequences by assigning degrees of homology to various substitutions, deletions, and other modifications. Conservative substitutions typically include substitutions within the following groups: glycine, alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid, asparagine,

10 glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine.

A nucleic acid molecule or polypeptide is said to be "substantially identical" to a reference molecule if it exhibits, over its entire length, at least 50%, 60%, or 70%, preferably at least 80% or 90%, more preferably at least 95%, and most preferably at least 99% identity to the sequence of the reference molecule. For polypeptides, the length of comparison sequences is at least 16 amino acids, preferably at least 20 amino acids or at least 25 amino acids, more preferably at least 35 amino acids, and most preferably, the full-length polypeptide. For nucleic acid molecules, the length of comparison sequences is at least 50 nucleotides, preferably at least 60 nucleotides, more preferably at least 75 nucleotides or at least 110 nucleotides, and most preferably, the full-length nucleic acid molecule. Alternatively, or additionally, two nucleic acid sequences are "substantially identical" if they hybridize under high stringency conditions.

By "isolated nucleic acid molecule," "substantially pure nucleic acid molecule," or "substantially pure and isolated nucleic acid molecule" is meant a nucleic acid molecule (for example, DNA) that is free of the genes that, in the naturally occurring genome of the organism from which the nucleic acid molecule of the invention is derived, flank the nucleic acid. The term includes, for example, a recombinant DNA that is incorporated

into a vector; into an autonomously replicating plasmid or virus; or into the genomic DNA of a prokaryote or eukaryote; or that exists as a separate molecule (e.g., a cDNA or a genomic or cDNA fragment produced by PCR or restriction endonuclease digestion) independent of other sequences. It
5 also includes a recombinant DNA that is part of a hybrid gene encoding additional polypeptide sequence.

By "antisense," as used herein in reference to nucleic acid molecules, is meant a molecule having a nucleic acid sequence, regardless of length, that is complementary to at least 75 nucleotides, and preferably at
10 least 100, 150, or 200 nucleotides, of the coding strand of a nucleic acid molecule encoding a prostate-specific or a testis-specific polypeptide, as described herein. An antisense molecule may also include regulatory sequences such as transcription enhancers, hormone responsive elements, ribosomal- and RNA polymerase binding sites, etc., which may be located
15 upstream or downstream of the coding region, and may have a distance of several ten base pairs to several ten thousand base pairs. An antisense nucleic acid molecule can be, for example, capable of preferentially lowering the production or expression of a prostate-specific or a testis-specific polypeptide encoded by a prostate-specific or a testis-specific
20 nucleic acid molecule.

By "prostate-specific" or "testis-specific" nucleic acid molecule is meant a nucleic acid molecule, such as a genomic DNA, cDNA, or RNA (e.g., mRNA) molecule, having at least 50, 60, or 75%, more preferably at least 80, 85, or 95%, and most preferably at least 99% amino acid identity
25 to the nucleic acid molecules described herein, for example, in Figures 4, 11, and 14. In addition, a nucleic acid molecule having at least 50, 60, or 75%, more preferably at least 80, 85, or 95%, and most preferably at least 99% nucleotide identity to a nucleotide sequence encoding amino acids 1-200 of STMP1 (SEQ ID NO: 14), preferably encoding amino acids 40-150

of STMP1, can be considered a prostate-specific or testis-specific nucleic acid molecule. Specifically excluded from this definition is STEAP (AF186249) (Hubert, R. S. et al., *Proc Natl Acad Sci U S A* 96, 14523-14528, 1999) and nucleic acid molecule sequences set forth in or encoding ESTs AF132025, AF177862, BAB23615, BAA91839, BAB15559, and NP_032190.

A preferred prostate-specific nucleic acid molecule may be preferentially expressed in prostate tissue at a level that is at least 5-fold higher, preferably at least 10-fold higher, more preferably at least 15-fold higher, and most preferably at least 20-fold higher than the level of the same nucleic acid molecule in at least one non-prostate tissue, preferably in all other non-prostate tissues. A prostate-specific nucleic acid molecule can also be expressed at high levels in a non-prostate tissue although, generally, the level of expression will be the highest in the prostate. Occasionally, as described herein, a prostate-specific nucleic acid molecule will be expressed at higher levels in non-prostate tissue (e.g., placenta, lung, or liver) than in the prostate.

A preferred testis-specific nucleic acid molecule may be preferentially expressed in testis tissue at a level that is at least 5-fold higher, preferably at least 10-fold higher, more preferably at least 15-fold higher, and most preferably at least 20-fold higher than the level of the same nucleic acid molecule in at least one non-testis tissue, preferably in all other non-testis tissues. A testis -specific nucleic acid molecule can also be expressed at high levels in a non-testis tissue although, generally, the level of expression will be the highest in the testis. Occasionally, as described herein, a testis -specific nucleic acid molecule will be expressed at higher levels in non-testis tissue (e.g., placenta, lung, or liver) than in the testis.

By "prostate-specific" or a "testis-specific" polypeptide or "prostate-specific" or a "testis-specific" protein is meant a polypeptide that is encoded by a prostate-specific or a testis-specific nucleic acid molecule. A prostate-specific or testis-specific polypeptide may also be defined as a 5 polypeptide having at least 50, 60, or 75%, more preferably at least 80, 85, or 95%, and most preferably at least 99% amino acid identity to the polypeptides described herein, for example, in Figures 4, 11, and 14. Specifically excluded from this definition is STEAP (AF186249) (Hubert, R. S. et al., *Proc Natl Acad Sci U.S.A.* 96, 14523-14528, 1999) and 10 polypeptide sequences set forth in or encoded by ESTs AF132025, AF177862, BAB23615, BAA91839, BAB15559, and NP_032190. In addition, a polypeptide having at least 50, 60, or 75%, more preferably at least 80, 85, or 95%, and most preferably at least 99% amino acid identity to amino acids 1-200 of STMP1 (SEQ ID NO: 14), preferably amino acids 15 40-150 of STMP1, can be considered a prostate-specific or testis-specific polypeptide.

A preferred prostate-specific polypeptide is preferentially expressed in prostate tissue at a level that is at least 5-fold higher, preferably at least 10-fold higher, more preferably at least 15-fold higher, and most preferably at least 20-fold higher than the level of the same polypeptide in at least one 20 non-prostate tissue, preferably in all other non-prostate tissues. A prostate-specific polypeptide can also be expressed at high levels in a non-prostate tissue although, generally, the level of expression will be the highest in the prostate. Occasionally, as described herein, a prostate-specific polypeptide 25 will be expressed at higher levels in non-prostate (e.g., placenta, lung, liver) than in the prostate.

A preferred testis-specific polypeptide is preferentially expressed in testis tissue at a level that is at least 5-fold higher, preferably at least 10-fold higher, more preferably at least 15-fold higher, and most preferably at

least 20-fold higher than the level of the same polypeptide in at least one non-testis tissue, preferably in all other non-testis tissues. A testis-specific polypeptide can also be expressed at high levels in a non-testis tissue although, generally, the level of expression will be the highest in the testis.

- 5 Occasionally, as described herein, a testis-specific polypeptide will be expressed at higher levels in non-testis (e.g., placenta, lung, liver) than in the testis.

The term prostate-specific or testis-specific polypeptide includes homologs, analogs, fragments, and isoforms, e.g., alternatively spliced isoforms, of the sequences described herein. By "biologically active fragment" is meant a polypeptide fragment of a prostate-specific or testis-specific polypeptide that exhibits, for example, extracellular trafficking, cell signaling, or other properties that are at least 30%, preferably at least 50%, more preferably at least 75%, and most preferably at least 100%, compared 10 with the properties of a full length prostate-specific or testis-specific polypeptide. By "analog" is meant any substitution, addition, or deletion in the amino acid sequence of a prostate-specific or testis-specific polypeptide that exhibits properties that are at least 30%, preferably at least 50%, more preferably at least 75%, and most preferably at least 100%, compared 15 with the extracellular trafficking or cell signaling properties of the polypeptide from which it is derived. Fragments, homologs, and analogs can be generated using standard techniques, for example, solid phase peptide synthesis or polymerase chain reaction. For example, point mutations may arise at any position of the sequence from an apurinic, apyrimidinic, or 20 otherwise structurally impaired site within the cDNA. Alternatively, point mutations may be introduced by random or site-directed mutagenesis 25 procedures (e.g., oligonucleotide assisted or by error prone PCR). Likewise, deletions and/or insertions may be introduced into the sequences, and preferred insertions comprise 5'- and/or 3'-fusions with a

polynucleotide that encodes a reporter moiety or an affinity moiety. Other preferred insertions comprise a nucleic acid that further includes functional elements such as a promoter, enhancer, hormone responsive element, origin of replication, transcription and translation initiation sites, etc. It should be
5 appreciated that where insertions with one or more functional elements are present, the resulting nucleic acid may be linear or circular (*e.g.*, transcription or expression cassettes, plasmids, etc.).

For use in the methods of the invention, the terms “prostate-specific” or “testis-specific” polypeptide further include the polypeptide sequences
10 set forth in or encoded by ESTs AF132025, AF177862, BAB23615, BAA91839, BAB15559, and NP_032190, but does not include STEAP, and a prostate-specific or testis-specific nucleic acid molecule includes the nucleotide sequences set forth in or encoding ESTs AF132025, AF177862, BAB23615, BAA91839, BAB15559, and NP_032190, but does not include
15 STEAP.

By “prostate-specific or a testis-specific gene or homolog or fragment thereof” is meant a gene; or homolog of a gene, that encodes a prostate-specific or testis-specific polypeptide.

By “specifically binds” is meant a compound, *e.g.*, an antibody, that
20 recognizes and binds a protein or polypeptide, for example, a prostate-specific or a testis-specific polypeptide, and that when detectably labeled can be competed away for binding to that protein or polypeptide by an excess of compound that is not detectably labeled. A compound that non-specifically binds is not competed away by excess detectably labeled
25 compound. A preferred antibody binds to any prostate-specific or a testis-specific polypeptide sequence that is substantially identical to any of the polypeptide sequences set forth in Figures 4, 11, and 14, or encoded by any of the nucleotide sequences set forth in Figures 3, 4, 11, and 14, or portions thereof.

By a "compound," "test compound," or "candidate compound" is meant a molecule, be it naturally-occurring or artificially-derived, and includes, for example, peptides, proteins, synthetic organic molecules, naturally-occurring organic molecules, nucleic acid molecules, and components thereof.

5 By "high stringency conditions" is meant conditions that allow hybridization comparable with the hybridization that occurs using a DNA probe of at least 500 nucleotides in length, in a buffer containing 0.5 M NaHPO₄, pH 7.2, 7% SDS, 1 mM EDTA, and 1% BSA (fraction V), at a 10 temperature of 65°C, or a buffer containing 48% formamide, 4.8X SSC, 0.2 M Tris-Cl, pH 7.6, 1X Denhardt's solution, 10% dextran sulfate, and 0.1% SDS, at a temperature of 42°C (these are typical conditions for high stringency Northern or Southern hybridizations). High stringency hybridization is also relied upon for the success of numerous techniques 15 routinely performed by molecular biologists, such as high stringency PCR, DNA sequencing, single strand conformational polymorphism analysis, and *in situ* hybridization. In contrast to Northern and Southern hybridizations, these techniques are usually performed with relatively short probes (e.g., usually 16 nucleotides or longer for PCR or sequencing, and 40 nucleotides 20 or longer for *in situ* hybridization). The high stringency conditions used in these techniques are well known to those skilled in the art of molecular biology, and may be found, for example, in Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, NY, 1998, hereby incorporated by reference.

25 By "probe" or "primer" is meant a single-stranded DNA or RNA molecule of defined sequence that can base pair to a second DNA or RNA molecule that contains a complementary sequence ("target"). The stability of the resulting hybrid depends upon the extent of the base pairing that occurs. This stability is affected by parameters such as the degree of

complementarity between the probe and target molecule, and the degree of stringency of the hybridization conditions. The degree of hybridization stringency is affected by parameters such as the temperature, salt concentration, and concentration of organic molecules, such as formamide, 5 and is determined by methods that are well known to those skilled in the art. Probes or primers specific for prostate-specific or a testis-specific nucleic acid molecules, preferably, have greater than 45% sequence identity, more preferably at least 55-75% sequence identity, still more preferably at least 75-85% sequence identity, yet more preferably at least 10 85-99% sequence identity, and most preferably 100% sequence identity to the nucleic acid sequences encoding the amino acid sequences described herein. Probes can be detectably-labeled, either radioactively or non-radioactively, by methods that are well-known to those skilled in the art. Probes can be used for methods involving nucleic acid hybridization, such 15 as nucleic acid sequencing, nucleic acid amplification by the polymerase chain reaction, single stranded conformational polymorphism (SSCP) analysis, restriction fragment polymorphism (RFLP) analysis, Southern hybridization, northern hybridization, *in situ* hybridization, electrophoretic mobility shift assay (EMSA), and other methods that are well known to 20 those skilled in the art.

A molecule, *e.g.*, an oligonucleotide probe or primer, a gene or fragment thereof, a cDNA molecule, a polypeptide, or an antibody, can be said to be "detectably-labeled" if it is marked in such a way that its presence can be directly identified in a sample. Methods for detectably-labeling molecules are well known in the art and include, without limitation, radioactive labeling (*e.g.*, with an isotope, such as ^{32}P or ^{35}S) and nonradioactive labeling (*e.g.*, with a fluorescent label, such as fluorescein, or by generating a construct containing green fluorescent protein (GFP)).

By "transgenic" is meant any cell that includes a DNA sequence or transgene that is inserted by artifice into a cell and becomes part of the genome of the organism that develops from that cell. As used herein, the transgenic organisms are generally transgenic mammals (e.g., mice, rats, and goats) and the DNA (transgene) is inserted by artifice into the nuclear genome. By "transgene" is meant any piece of DNA that is inserted by artifice into a cell, and becomes part of the genome of the organism that develops from that cell. Such a transgene may include a gene that is partly or entirely heterologous (i.e., foreign) to the transgenic organism, or may represent a gene homologous to an endogenous gene of the organism.

By "knockout mutation" is meant an artificially induced alteration in the nucleic acid sequence (created via recombinant DNA technology or deliberate exposure to a mutagen) that reduces the biological activity of the polypeptide normally encoded therefrom by at least 80% relative to the unmutated gene. The mutation may, without limitation, be an insertion, deletion, frameshift mutation, or a missense mutation. The knockout mutation can be in a cell *ex vivo* (e.g., a tissue culture cell or a primary cell) or *in vivo*. A "knockout animal" is a mammal, preferably, a mouse, containing a knockout mutation as defined above.

By "sample" is meant a tissue biopsy, cells, blood, serum, urine, stool, or other specimen obtained from a patient or test subject. The sample is analyzed to detect a mutation in a gene encoding a prostate-specific or a testis-specific polypeptide, or expression levels of a gene encoding a prostate-specific or a testis-specific polypeptide, as for example, an indication of the progression of cancer, by methods that are known in the art or described herein. For example, methods such as sequencing, single-strand conformational polymorphism (SSCP) analysis, or restriction fragment length polymorphism (RFLP) analysis of PCR products derived from a patient sample may be used to detect a mutation in a gene encoding

a prostate-specific or a testis-specific polypeptide; ELISA may be used to measure levels of a prostate-specific or a testis-specific polypeptide; and PCR may be used to measure the level of nucleic acids encoding a prostate-specific or a testis-specific polypeptide.

5 By "pharmaceutically acceptable carrier" is meant a carrier that is physiologically acceptable to the treated mammal while retaining the therapeutic properties of the compound with which it is administered. One exemplary pharmaceutically acceptable carrier is physiological saline solution. Other physiologically acceptable carriers and their formulations
10 are known to one skilled in the art and described, for example, in *Remington: The Science and Practice of Pharmacy*, (19th edition), ed. A. Gennaro, 1995, Mack Publishing Company, Easton, PA.

"Therapeutically effective amount" as used herein in reference to dosage of a medication, refers to the administration of a specific amount of
15 a pharmacologically active agent (e.g., a prostate-specific or a testis-specific polypeptide, nucleic acid molecule, or modulatory compound) tailored to each individual patient manifesting symptoms characteristic of a specific disorder. For example, a patient receiving the treatment of the present invention might have prostate cancer. A person skilled in the art
20 will recognize that the optimal dose of a pharmaceutical agent to be administered will vary from one individual to another. Dosage in individual patients should take into account the patients height, weight, rate of absorption and metabolism of the medication in question, the stage of the disorder to be treated, and what other pharmacological agents are
25 administered concurrently.

By "treating" or "treatment" is meant the medical management of a patient with the intent to cure, ameliorate, stabilize, or prevent a disease, pathological condition, or disorder. This term includes active treatment, that is, treatment directed specifically toward the improvement or

- associated with the cure of a disease, pathological condition, or disorder, and also includes causal treatment, that is, treatment directed toward removal of the cause of the associated disease, pathological condition, or disorder. In addition, this term includes palliative treatment, that is,
- 5 treatment designed for the relief of symptoms rather than the curing of the disease, pathological condition, or disorder; preventative treatment, that is, treatment directed to minimizing or partially or completely inhibiting the development of the associated disease, pathological condition, or disorder; and supportive treatment, that is, treatment employed to supplement
- 10 another specific therapy directed toward the improvement of the associated disease, pathological condition, or disorder. The phrase "treatment" also includes symptomatic treatment, that is, treatment directed toward constitutional symptoms of the associated disease, pathological condition, or disorder.
- 15 By "disorder of the prostate or testis" is meant a disturbance of function and/or structure of the prostate or testis in a living organism, resulting from an external source, a genetic predisposition, a physical or chemical trauma, or a combination of the above. Such disorders include the proliferation of prostate or testicular cells. By "cell proliferation" is meant the growth or reproduction of similar cells, and the invention provides reagents for inhibiting proliferation and stimulating proliferation. By "inhibiting proliferation" is meant the decrease in the number of similar cells by at least 10%, more preferably by at least 20%, and most preferably by at least 50%. By "stimulating proliferation" is meant an increase in the
- 20 number of similar cells by at least 10%, more preferably by at least 20%, and most preferably by at least 50%.
- 25

The reagents described herein, for example, vectors expressing antisense, antagonists, or inhibitors of prostate-specific or testis-specific polypeptides or nucleic acid molecules may be used, for example, to

suppress the excessive proliferation of prostate or testicular cells. Blocking prostate-specific or testis-specific polypeptide or nucleic acid molecule expression or activity in prostate or testicular cells can alter molecular pathways within cancerous cells and thus trigger apoptosis, i.e., the process 5 of cell death where a dying cell displays a set of well-characterized biochemical hallmarks which include cytolemmal blebbing, cell soma shrinkage, chromatin condensation, and DNA laddering.

Disorders of the prostate or testis include prostate cancer, benign prostatic hyperplasia, acute prostatitis, testicular cancer, developmental 10 defects of the prostate or testis (such as cryptorchidism or undescended testis, and retractile, ascending, or vanished testis).

By "proliferative disease" is meant a disease that is caused by or results in inappropriately high levels of cell division, inappropriately low levels of apoptosis, or both. For example, cancers such as prostate cancer, 15 testicular cancer, lymphoma, leukemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer, and lung cancer are all examples of proliferative disease.

By "modulate" or "modulating" is meant changing, either by decrease or increase, the expression or biological activity of a prostate- 20 specific or testis-specific nucleic acid molecule or polypeptide, as described herein. It will be appreciated that the degree of modulation provided by a modulating compound in a given assay will vary, but that one skilled in the art can determine the statistically significant change in the level of biological activity that identifies a compound that modulates a prostate- 25 specific or testis-specific nucleic acid molecule or polypeptide.

The invention provides several advantages. For example, it provides methods and reagents that can be used in the diagnosis and treatment of prostate and testis associated diseases, as well as other disorders and conditions that are sensitive to the bioactivities of the reagents (e.g.,

polypeptides, nucleic acid molecules, antibodies) described herein. Since the prostate-specific or testis-specific polypeptides of the invention have been found to be highly expressed in the prostate and testis, these polypeptides can also be used in screens for therapeutics to treat disorders 5 associated with the prostate and testis. These polypeptides are also expressed in other tissues, and can be used as therapeutics and diagnostics for cell proliferative disorders.

Other features and advantages of the invention will be apparent from the detailed description of the invention, the drawings, and the claims.

10

Brief Description of The Drawings

Figure 1 shows an exemplary reverse northern analysis of several clones from a prostate specific cDNA library.

Figure 2 shows an exemplary multiple tissue northern blot.

15

Figure 3 is a table showing the nucleotide sequences of twelve clones (SEQ ID NOs: 1-12) isolated from prostate tissue and LNCaP cells .

Figure 4A is a schematic diagram showing the *STMP1* gene structure.

Figure 4B shows the nucleotide sequence, including the intron 20 junction sequences (SEQ ID NO: 13), and predicted amino acid sequence (SEQ ID NO: 14) of STMP1.

Figure 4C shows the nucleotide sequences of the exons and 3' UTR of *STMP1* (SEQ ID NOs: 15-21).

25

Figure 4D shows the nucleotide sequence of the ORF of *STMP1* (SEQ ID NO: 22).

Figure 4E shows the shows the cDNA sequence (SEQ ID NO: 23), and predicted amino acid sequence (SEQ ID NO:14) of STMP1.

Figure 4F shows the nucleotide sequences of the exons and 3' UTR of *STMP1* ORF2 (SEQ ID NOs: 17-20 and 24-26).

Figure 4G shows the nucleotide sequence of the ORF of *STMP1* ORF2 (SEQ ID NO: 27).

Figure 4H shows the cDNA sequence (SEQ ID NO: 28), and predicted amino acid sequence (SEQ ID NO: 29) of *STMP1* ORF2.

5 Figure 4I shows the nucleotide sequences of the exons and 3' UTR of *STMP1* ORF3 (SEQ ID NOs: 17-19 and 24-26).

Figure 4J shows the nucleotide sequence of the ORF of *STMP1* ORF3 (SEQ ID NO: 30).

10 Figure 4K shows the cDNA sequence (SEQ ID NO: 31), and predicted amino acid sequence (SEQ ID NO: 32) of *STMP1* ORF3.

Figure 4L shows the cDNA sequence (SEQ ID NO: 33), and predicted amino acid sequence (SEQ ID NO: 34) of *STMP2*.

Figure 4M shows the cDNA sequence (SEQ ID NO: 35), and predicted amino acid sequence (SEQ ID NO: 36) of *STMP3*.

15 Figure 5 shows a sequence alignment of *STMP1* (SEQ ID NO: 14), with STEAP (SEQ ID NO: 37, Accession No. AF186249), and two ESTs (Accession No. BAA91839 and Accession No. BAB15559; SEQ ID NOs: 38 and 39, respectively).

Figure 6A shows a multiple tissue Northern blot probed with *STMP1* or *G3PDH* cDNA.

20 Figure 6B is a Northern blot probed with *STMP1* and *PSA* in the androgen-responsive prostate cancer cell line LNCaP and in the CWR22 human prostate cancer xenograft model.

25 Figure 6C is a Northern blot probed with *STMP1* and *NKX3A* in LNCaP, PC-3, and DU-145 cell lines and in the CWR22R human prostate cancer xenograft model.

Figure 7A shows fluorescence microscopy images of COS-1 cells transiently transfected with GFP-*STMP1*.

Figure 7B shows fluorescence microscopy images of COS-1 cells transiently transfected with GFP-STMP1 and labeled with antibodies against Golgi markers.

5 Figure 8 shows fluorescence microscopy images of COS-1 cells transiently transfected with GFP-STMP1 and observed by live-cell confocal microscopy.

Figure 9 shows fluorescence microscopy images of COS-1 cells transiently transfected with GFP-STMP1 and labeled with an antibody against an early endosomal marker.

10 Figure 10 is a schematic diagram showing the *SSH9* gene structure and two mRNA species transcribed from the *SSH9* gene.

Figure 11A shows the cDNA (SEQ ID NO: 40) and predicted amino acid sequence (SEQ ID NO: 41) for *SSH9*.

15 Figure 11B shows the predicted promoter sequence for *SSH9* (SEQ ID NO: 42).

Figure 11C shows the predicted intron-exon boundaries for *SSH9* (SEQ ID NOs: 43-50).

20 Figure 12A is a Northern blot probed with *SSH9* in the androgen-responsive prostate cancer cell line LNCaP cells and in the CWR22 human prostate cancer xenograft model.

Figure 12B is a Northern blot probed with *SSH9* in LNCaP, PC-3, and DU-145 cell lines, and CWR22R human prostate cancer xenograft model.

25 Figure 12C is a multiple tissue Northern blot probed with *SSH9* or *GAPDH* cDNA.

Figure 13 is a schematic diagram showing the *PSL22* gene structure.

Figure 14A shows the nucleotide sequence of the ORF of *PSL22* (SEQ ID NO: 51).

Figure 14B shows the cDNA sequence (SEQ ID NO: 52), and predicted amino acid sequence (SEQ ID NO: 53) of PSL22.

Figure 14C shows the nucleotide sequences of the TATA promoter and transcription start site, exons, and 5' and 3' UTRs of *PSL22* (SEQ ID NOs: 54-70).

Figure 15 shows a sequence alignment of PSL22 (RhoBP) (SEQ ID NO: 53), with ESTs NP032190 (mRhoph), AF132025 (dRhoph), and BAB23615 (SEQ ID Nos:71-73).

Figure 16A is a Northern blot probed with *PSL22* in LNCaP, PC-3, 10 and DU-145 cell lines, and in the CWR22R human prostate cancer xenograft model.

Figure 16B is a multiple tissue Northern blot probed with *PSL22* cDNA.

15 Detailed Description of the Invention

The basic biology of the normal prostate and testis, as well as prostate and testicular cancer initiation and progression is still poorly understood. It is therefore necessary to delineate the molecular events that are at the basis of these processes. To achieve this goal, we have 20 identified, cloned, and characterized highly prostate- and testis-enriched genes whose gene products have important roles for both the normal physiology and the pathophysiology of the prostate and the testis. These gene products also have important roles in other disorders, for example, heart, brain, liver, pancreas, kidney, and colon, which are the tissues where 25 variable low expression, and occasionally, very high expression of specific gene products, can be detected by Northern analysis.

The invention provides prostate-specific or testis-specific polypeptides and nucleic acid molecules (see below), and diagnostic and therapeutic methods employing these polypeptides and nucleic acid

molecules. The invention also provides methods for identifying compounds that modulate the biological activities of prostate-specific or testis-specific polypeptides and nucleic acid molecules, and therapeutic methods employing these compounds. The diagnostic, therapeutic, and screening methods of the invention are first described, followed by general approaches that can be used in carrying out these methods. Finally, experimental results supporting the methods of the invention are described.

Bioassays

Prostate-specific and testis-specific polypeptides are expressed in the prostate and testis, and also in other tissues such as kidney, pancreas, liver, lung, and colon. The expression patterns of prostate-specific and testis-specific polypeptides in specific cells and tissues are used to identify cellular targets of prostate-specific and testis-specific polypeptide actions, and to identify bioactivities that are relevant to specific prostate- and testis-related diseases, such as prostate cancer, testicular cancer, benign prostatic hyperplasia, acute prostatitis, and developmental testis defects.

Therapeutic and diagnostic utilities for prostate-specific and testis-specific polypeptides are identified by, for example, conducting bioassays *in vitro*. Culture systems that reflect prostate-specific and testis-specific polypeptide expression patterns, along with the distribution of particular receptors, such as the androgen receptor, are selected. For example, LNCaP cells express androgen receptors, and respond to one or more isoforms of prostate-specific and testis-specific polypeptides in a variety of bioassays. The activities of prostate-specific and testis-specific polypeptides (*e.g.*, STMP1, SSH9, PSL22) are compared, using sister cultures, in various dose-response assays, including but not limited to, inhibition of proliferation, apoptosis, signaling events (*e.g.* changes in kinase activity), changes in transcription factor activity (such as that of the androgen receptor), intracellular trafficking, or cell signaling. The relative

potencies of the prostate-specific and testis-specific polypeptides are determined on the basis of, for example, protein concentration.

Diagnostic Methods Employing Prostate-Specific Or Testis-Specific

5 Nucleic Acid Molecules, Polypeptides, and Antibodies

Prostate-specific or testis-specific nucleic acid molecules, polypeptides, and antibodies are used in methods to diagnose or monitor a variety of diseases and conditions, including those involving mutations in, or inappropriate expression of, prostate-specific or testis-specific genes.

10 Prostate-specific or testis-specific expression has been documented in a variety of tissues, as discussed above. Thus, detection of abnormalities in prostate-specific or testis-specific genes or their expression is used in methods to diagnose, or to monitor treatment or development of diseases of these tissues.

15 The diagnostic methods of the invention are used, for example, with patients that have a prostate-related or testis-related disease, for example, prostate or testicular cancer, in an effort to determine its etiology, and thus, to facilitate selection of an appropriate course of treatment. The diagnostic methods are also used with patients that have not yet developed a prostate-
20 related or testis-related disease, but who may be at risk of developing such a disease, or with patients that are at an early stage of developing such a disease. Many prostate-related or testis-related diseases occur during development, and thus, the diagnostic methods of the invention are also carried out on a fetus or embryo during development. Also, the diagnostic
25 methods of the invention are used in prenatal genetic screening, for example, to identify parents who may be carriers of a recessive prostate-related or testis-related mutation.

Prostate-specific or testis-specific abnormalities that are detected using the diagnostic methods of the invention include those characterized

by, for example, (i) abnormal prostate-specific or testis-specific polypeptides, (ii) prostate-specific or testis-specific genes containing mutations that result in the production of such polypeptides, and (iii) mutations that result in production of abnormal amounts of prostate-specific or testis-specific polypeptides.

Levels of prostate-specific or testis-specific expression in a patient sample are determined by using any of a number of standard techniques that are well known in the art. For example, prostate-specific or testis-specific expression in a biological sample (e.g., a blood, prostate or testis tissue sample, or amniotic fluid) from a patient is monitored by standard northern blot analysis or by quantitative PCR (see, e.g., Ausubel *et al.*, *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, NY, 1998; *PCR Technology: Principles and Applications for DNA Amplification*, H.A. Ehrlich, Ed., Stockton Press, NY; Yap *et al.* *Nucl. Acids. Res.* 19:4294, 1991).

A biological sample obtained from a patient can be analyzed for one or more mutations in prostate-specific or testis-specific nucleic acid molecules using a mismatch detection approach. Generally, this approach involves PCR amplification of nucleic acid molecules from a patient sample, followed by identification of a mutation (*i.e.*, a mismatch) by detection of altered hybridization, aberrant electrophoretic gel migration, binding, or cleavage mediated by mismatch binding proteins, or by direct nucleic acid molecule sequencing. Any of these techniques can be used to facilitate detection of mutant prostate-specific or testis-specific genes, and each is well known in the art. Examples of these techniques are described, for example, by Orita *et al.* (*Proc. Natl. Acad. Sci. USA* 86:2766-2770, 1989) and Sheffield *et al.* (*Proc. Natl. Acad. Sci. USA* 86:232-236, 1989).

Mismatch detection assays also provide an opportunity to diagnose a prostate-specific or testis-specific gene-mediated predisposition to a disease

before the onset of symptoms. For example, a patient heterozygous for a prostate-specific or testis-specific mutation that suppresses normal prostate-specific or testis-specific biological activity or expression may show no clinical symptoms of a prostate-specific or testis-specific gene-related disease, and yet possess a higher than normal probability of developing a prostate or testicular disease. Given such a diagnosis, patients can take precautions to minimize their exposure to adverse environmental factors and to carefully monitor their medical condition (for example, through frequent physical examinations). As mentioned above, this type of diagnostic approach can also be used to detect prostate-specific or testis-specific mutations in prenatal screens.

The prostate-specific or testis-specific diagnostic assays described above can be carried out using any biological sample (for example, a blood, prostate, or testis tissue sample, or amniotic fluid) in which a prostate-specific or testis-specific polypeptide or nucleic acid molecule is normally expressed. A mutant prostate-specific or testis-specific gene can also be identified using these sources as test samples. Alternatively, a prostate-specific or testis-specific mutation, as part of a diagnosis for predisposition to a prostate-specific or testis-specific gene-associated disease, can be tested for using a DNA sample from any cell, for example, by mismatch detection techniques. Preferably, the DNA sample is subjected to PCR amplification prior to analysis.

In yet another diagnostic approach of the invention, an immunoassay is used to detect or monitor prostate-specific or testis-specific protein expression in a biological sample. Anti-prostate-specific or testis-specific--polypeptide polyclonal or monoclonal antibodies (as described below) can be used in any standard immunoassay format (*e.g.*, ELISA, Western blot, or RIA; see, *e.g.*, Ausubel *et al.*, *supra*) to measure prostate-specific or testis-specific polypeptide levels. These levels are compared to wild-type

prostate-specific or testis-specific levels. For example, an increase in prostate-specific or testis-specific polypeptide production may be indicative of a condition or a predisposition to a condition involving overexpression of prostate-specific or testis-specific polypeptide biological activity, such as
5 late stage prostate cancer.

Immunohistochemical techniques can also be utilized for prostate-specific or testis-specific polypeptide detection. For example, a tissue sample can be obtained from a patient, sectioned, and stained for the presence of prostate-specific or testis-specific polypeptide using an anti-
10 prostate-specific or testis-specific antibody (see below) and any standard detection system (e.g., one that includes a secondary antibody conjugated to horseradish peroxidase). General guidance regarding such techniques can be found in, e.g., Bancroft *et al.*, *Theory and Practice of Histological Techniques*, Churchill Livingstone, 1982, and Ausubel *et al.*, *supra*.

15 In a preferred example, a combined diagnostic method can be employed that includes an evaluation of prostate-specific or testis-specific protein production (for example, by immunological techniques or the protein truncation test (Hogerhorst *et al.*, *Nature Genetics* 10:208-212, 1995), and a nucleic acid molecule-based detection technique designed to
20 identify more subtle prostate-specific or testis-specific mutations (for example, point mutations). As described above, a number of mismatch detection assays are available to those skilled in the art, and any preferred technique can be used. Mutations in prostate-specific or testis-specific genes can be detected that either result in loss or gain of prostate-specific or
25 testis-specific polypeptide or nucleic acid molecule expression or loss or gain of normal prostate-specific or testis-specific polypeptide or nucleic acid molecule biological activity.

Prostate-specific or testis-specific polypeptides or nucleic acid molecules can be used to correlate the course of prostate cancer to a marker

other than PSA, to monitor the course of an anticancer therapy, or to detect a neoplastic cell in a system. For example, a predetermined quantity of an RNA encoding a prostate-specific or testis-specific polypeptide is correlated with the presence of a neoplastic cell, for example, from a
5 biopsy. The total RNA is extracted from the biopsy specimen, and a real time quantitative rt-PCR employing individual reactions with primer pairs specific to prostate-specific or testis-specific sequences is performed in parallel with a biopsy specimen known to be free of cancer cells. Biopsy specimens are determined to have a cancer cell, where the detected
10 prostate-specific or testis-specific mRNA quantity is at least 5 times higher than in the control specimen. An exemplary extraction of total RNA utilizes the Quiagen BioRobot kit in conjunction with the BioRobot 9600 system, and the real time rtPCR is performed in a Perkin Elmer ABI Prism 7700.

15 In alternative aspects of the inventive subject matter, the method of
detecting a neoplastic cell need not be limited to biopsy tissues from
prostate or testis tissue, but may employ various alternative tissues,
including lymphoma tumor cells, and various solid tumor cells, so long as
such tumor cells overproduce mRNA of prostate-specific or testis-specific
20 polypeptides. Appropriate alternative tumor cells can readily be identified
by the above described method. Likewise, the system need not be restricted
to a mammal, but may also include cell-, and tissue cultures grown *in vitro*,
and tumor cells and specimens from animals other than mammals. For
example, tumor cell and tissue grown *in vitro* may advantageously be
25 utilized to investigate drug action on such cells, and sequences encoding
prostate-specific or testis-specific polypeptides may conveniently be
employed as tumor marker. Alternatively, body fluids (e.g., serum, saliva,
etc.) that may or may not contain tumor cells are also contemplated a
suitable substrate for the method presented herein, so long as they contain

to at least some extent mRNA encoding a prostate-specific or testis-specific polypeptide.

In still other aspects of contemplated methods, the polypeptide quantity need not necessarily be limited to at least 5 times more than the 5 control specimen in order to establish that the tissue has a cancer cell. For example, where the concentration of the polypeptide is hormone dependent, amounts between 3-8 fold and more may be appropriate. In contrast, where the concentration of cancer cells in the biopsy specimen is relatively low, amounts of less than 5-fold, including 1.5 to 4.9-fold and less are 10 contemplated.

The detection process may include fluorescence detection, luminescence detection, scintigraphy, autoradiography, and formation of a dye. For example, for microscopic analysis of biopsy specimens, luciferase labeled probes are particularly advantageous in conjunction with a 15 luminescence substrate (*e.g.*, luciferin). Luminescence quantification may then be performed utilizing a CCD-camera and image analysis system. Similarly, radioactivity may be detected via autoradiographic or scintigraphic procedures on a tissue section, in a fluid or on a solid support. Where the probe is a natural or synthetic ligand of a prostate-specific or 20 testis-specific polypeptide, the ligand may include molecules with a chemical modification that increase the affinity to the polypeptide and/or induce irreversible binding to the polypeptide. For example, transition state analogs or suicide inhibitors for a particular reaction catalyzed by the polypeptide are especially contemplated. Labeling of antibodies, antibody 25 fragments, small molecules, and binding of the labeled entity is a technique that is well known in the art, and all known methods are generally suitable for use in conjunction with methods contemplated herein. Furthermore, the probe need not be limited to a fluorescein labeled antibody, and alternative probes include antibody fragments (*e.g.*, Fab, Fab', scFab, etc.).

- Still further contemplated variations include substitution of one or more atoms or chemical groups in the sequence with a radioactive atom or group. For example, where cDNAs are employed as a hybridization-specific probes, a fluorophor or enzyme (*e.g.*, β -galactosidase for
- 5 generation of a dye, or luciferase for generation of luminescence) may be coupled to the sequence to identify position and/or quantity of a complementary sequence. Alternatively, where contemplated cDNA molecules are utilized for affinity isolation procedures, the cDNA may be coupled to a molecule that is known to have a high-affinity (*i.e.*, $K_d < 10^4 \text{ mol}^{-1}$) partner,
- 10 such as biotin, or an oligo-histidyl tag. In another example, one or more phosphate groups may be exchanged for a radioactive phosphate group with a ^{32}P or ^{33}P isotope to assist in detection and quantification, where the radiolabeled cDNA is employed as a hybridization probe.
- 15 **Therapeutic Methods Employing Prostate-Specific Or Testis-Specific Nucleic Acid Molecules, Polypeptides, and Antibodies**
- The invention includes methods of treating or preventing prostate-specific or testis-specific diseases. Therapies are designed to circumvent or overcome a prostate-specific or testis-specific gene defect, or inadequate or
- 20 excessive prostate-specific or testis-specific gene expression, and thus modulate and possibly alleviate conditions involving defects in prostate-specific or testis-specific genes or proteins. In considering various therapies, it is understood that such therapies are, preferably, targeted to the affected or potentially affected organs, for example, the prostate or the
- 25 testis. Reagents that are used to modulate prostate-specific or testis-specific biological activity can include, without limitation, full length prostate-specific or testis-specific polypeptides; prostate-specific or testis-specific cDNA, mRNA, or antisense RNA; prostate-specific or testis-specific antibodies; and any compound that modulates prostate-specific or

testis-specific polypeptide or nucleic acid molecule biological activity, expression, or stability.

- Treatment or prevention of diseases resulting from a mutated prostate-specific or testis-specific gene is accomplished, for example, by
- 5 replacing a mutant prostate-specific or testis-specific gene with a normal prostate-specific or testis-specific gene, administering a normal prostate-specific or testis-specific gene, modulating the function of a mutant prostate-specific or testis-specific protein, delivering normal prostate-specific or testis-specific protein to the appropriate cells, or altering the
- 10 levels of normal or mutant prostate-specific or testis-specific protein. It is also possible to correct a prostate-specific or testis-specific gene defect to modify the physiological pathway (*e.g.*, an intracellular trafficking pathway) in which the prostate-specific or testis-specific protein participates.

- 15 To replace a mutant protein with normal protein, or to add protein to cells that do not express sufficient or normal prostate-specific or testis-specific protein, it may be necessary to obtain large amounts of pure prostate-specific or testis-specific protein from cultured cell systems in which the protein is expressed (*see, e.g.*, below). Delivery of the protein to the affected tissue can then be accomplished using appropriate packaging or administrating systems. Alternatively, small molecule analogs that act as prostate-specific or testis-specific molecule agonists or antagonists can be administered to produce a desired physiological effect (*see below*).

- 20 Gene therapy is another therapeutic approach for preventing or ameliorating diseases caused by prostate-specific or testis-specific gene defects. Nucleic acid molecules encoding wild type prostate-specific or testis-specific proteins can be delivered to cells that lack sufficient, normal prostate-specific or testis-specific biological activity (*e.g.*, cells carrying mutations in prostate-specific or testis-specific genes). The nucleic acid

molecules must be delivered to those cells in a form in which they can be taken up by the cells and so that sufficient levels of protein, to provide effective prostate-specific or testis-specific function, can be produced.

Alternatively, for some prostate-specific or testis-specific mutations, it may
5 be possible slow the progression of the resulting disease or to modulate prostate-specific or testis-specific activity by introducing another copy of a homologous gene bearing a second mutation in that gene, to alter the mutation, or to use another gene to block any negative effect.

Transducing retroviral, adenoviral, and adeno-associated viral
10 vectors can be used for somatic cell gene therapy, especially because of their high efficiency of infection and stable integration and expression (see, e.g., Cayouette *et al.*, *Human Gene Therapy* 8:423-430, 1997; Kido *et al.*, *Current Eye Research* 15:833-844, 1996; Bloomer *et al.*, *Journal of Virology* 71:6641-6649, 1997; Naldini *et al.*, *Science* 272:263-267, 1996;
15 and Miyoshi *et al.*, *Proc. Natl. Acad. Sci., USA* 94:10319-1032, 1997). For example, the full length prostate-specific or testis-specific gene, or a portion thereof, can be cloned into a retroviral vector and expression can be driven from its endogenous promoter, from the retroviral long terminal repeat, or from a promoter specific for a target cell type of interest (such as aortic or other vascular cells). Other viral vectors that can be used include, for example, vaccinia virus, bovine papilloma virus, or a herpes virus, such as Epstein-Barr Virus (also see, for example, the vectors of Miller, *Human Gene Therapy* 15-14, 1990; Friedman, *Science* 244:1275-1281, 1989; Eglitis *et al.*, *BioTechniques* 6:608-614, 1988; Tolstoshev *et al.*, *Current
20 Opinion in Biotechnology* 1:55-61, 1990; Sharp, *The Lancet* 337:1277-1278, 1991; Cornetta *et al.*, *Nucleic Acid Research and Molecular Biology* 36:311-322, 1987; Anderson, *Science* 226:401-409, 1984; Moen, *Blood Cells* 17:407-416, 1991; or Miller *et al.*, *Biotechnology* 7:980-990, 1989).
25 Retroviral vectors are particularly well developed and have been used in

clinical settings (Rosenberg *et al.*, *N. Engl. J. Med.* 323:370, 1990; Anderson *et al.*, U.S. Patent No. 5,399,346).

- Gene transfer can also be achieved using non-viral means involving transfection *in vitro*, by means of any standard technique, including but not limited to, calcium phosphate, DEAE dextran, electroporation, protoplast fusion, and liposomes. Transplantation of normal genes into the affected tissues of a patient can also be accomplished by transferring a normal prostate-specific or testis-specific gene into a cultivatable cell type *ex vivo*, after which the cell (or its descendants) is injected into a targeted tissue.
- Another strategy for inhibiting prostate-specific or testis-specific function using gene therapy involves intracellular expression of an anti-prostate-specific or testis-specific antibody or a portion of an prostate-specific or testis-specific antibody. For example, the gene (or gene fragment) encoding a monoclonal antibody that specifically binds to prostate-specific or testis-specific polypeptide and inhibits its biological activity is placed under the transcriptional control of a tissue-specific gene regulatory sequence. Another therapeutic approach involves administration of recombinant prostate-specific or testis-specific polypeptide, either directly to the site of a potential or actual disease-affected tissue (for example, by injection) or systemically (for example, by any conventional recombinant protein administration technique). The dosage of a prostate-specific or testis-specific polypeptide depends on a number of factors, including the size and health of the individual patient but, generally, between about 0.006 mg/kg to about 0.6 mg/kg, inclusive, is administered per day to an adult in any pharmaceutically acceptable formulation.

Non-viral approaches can also be employed for the introduction of therapeutic DNA into cells predicted to be subject to diseases involving a prostate-specific or testis-specific disorder. For example, a prostate-specific or testis-specific nucleic acid molecule or an antisense nucleic acid

molecule can be introduced into a cell by lipofection (Felgner *et al.*, *Proc. Natl. Acad. Sci. USA* 84:7413, 1987; Ono *et al.*, *Neuroscience Letters* 17:259, 1990; Brigham *et al.*, *Am. J. Med. Sci.* 298:278, 1989; Staubinger *et al.*, *Methods in Enzymology* 101:512, 1983), asialoorosomucoid-polylysine conjugation (Wu *et al.*, *Journal of Biological Chemistry* 263:14621, 1988; Wu *et al.*, *Journal of Biological Chemistry* 264:16985, 1989), or, less preferably, micro-injection under surgical conditions (Wolff *et al.*, *Science* 247:1465, 1990).

Prostate-specific or testis-specific cDNA expression for use in gene therapy methods can be directed from any suitable promoter (*e.g.*, the human cytomegalovirus (CMV), simian virus 40 (SV40), or metallothionein promoters), and regulated by any appropriate mammalian regulatory element. For example, if desired, enhancers known to preferentially direct gene expression in specific cell types can be used to direct prostate-specific or testis-specific expression. The enhancers used can include, without limitation, those that are characterized as tissue- or cell-specific enhancers. Alternatively, if a prostate-specific or testis-specific genomic clone is used as a therapeutic construct (such clones can be identified by hybridization with prostate-specific or testis-specific cDNA, described above), regulation can be mediated by the cognate regulatory sequences, or, if desired, by regulatory sequences derived from a heterologous source, including any of the promoters or regulatory elements described above.

Antisense-based strategies can be employed to explore prostate-specific or testis-specific gene function and as a basis for therapeutic drug design. These strategies are based on the principle that sequence-specific suppression of gene expression (via transcription or translation) can be achieved by intracellular hybridization between genomic DNA or mRNA and a complementary antisense species. The formation of a hybrid RNA

duplex interferes with transcription of the target prostate-specific or testis-specific-encoding genomic DNA molecule, or processing, transport, translation, or stability of the target prostate-specific or testis-specific mRNA molecule.

5 Antisense strategies can be delivered by a variety of approaches. For example, antisense oligonucleotides or antisense RNA can be directly administered (*e.g.*, by intravenous injection) to a subject in a form that allows uptake into cells. Alternatively, viral or plasmid vectors that encode antisense RNA (or antisense RNA fragments) can be introduced into a cell
10 *in vivo* or *ex vivo*. Antisense effects can be induced by control (sense) sequences; however, the extent of phenotypic changes are highly variable. Phenotypic effects induced by antisense effects are based on changes in criteria such as protein levels, protein activity measurement, and target mRNA levels.

15 For example, prostate-specific or testis-specific gene therapy can also be accomplished by direct administration of antisense prostate-specific or testis-specific mRNA to a cell that is expected to be adversely affected by the expression of wild-type or mutant prostate-specific or testis-specific polypeptides. The antisense prostate-specific or testis-specific mRNA can
20 be produced and isolated by any standard technique, but is most readily produced by *in vitro* transcription using an antisense prostate-specific or testis-specific cDNA under the control of a high efficiency promoter (*e.g.*, the T7 promoter). Administration of antisense prostate-specific or testis-specific mRNA to cells can be carried out by any of the methods for direct
25 nucleic acid molecule administration described above.

An alternative strategy for inhibiting prostate-specific or testis-specific function using gene therapy involves intracellular expression of an anti-prostate-specific or testis-specific antibody or a portion of an anti-

prostate-specific or testis-specific antibody. For example, the gene (or gene fragment) encoding a monoclonal antibody that specifically binds to prostate-specific or testis-specific and inhibits its biological activity can be placed under the transcriptional control of a tissue-specific gene regulatory sequence.

5 Another therapeutic approach within the invention involves administration of recombinant prostate-specific or testis-specific polypeptide, either directly to the site of a potential or actual disease-affected tissue (for example, by injection) or systemically (for example, by 10 any conventional recombinant protein administration technique). The dosage of prostate-specific or testis-specific depends on a number of factors, including the size and health of the individual patient, but, generally, between 0.1 mg and 100 mg, inclusive, are administered per day to an adult in any pharmaceutically acceptable formulation.

15 In a patient diagnosed as having a prostate-specific or testis-specific mutation gene or a prostate-specific or testis-specific disease, or as susceptible to prostate-specific or testis-specific gene mutations, aberrant prostate-specific or testis-specific polypeptide or nucleic acid molecule expression (even if those mutations or expression patterns do not yet result 20 in alterations in prostate-specific or testis-specific expression or biological activity), or to a prostate-specific or testis-specific disease, any of the above-described therapies are administered before the occurrence of the disease phenotype. Also, compounds shown to modulate prostate-specific or testis-specific polypeptide or nucleic acid molecule expression or 25 prostate-specific or testis-specific polypeptide or nucleic acid molecule biological activity are administered to patients diagnosed with potential or actual diseases by any standard dosage and route of administration.

Alternatively, gene therapy using an antisense prostate-specific or testis-

specific mRNA expression construct is undertaken to reverse or prevent the gene defect prior to the development of the full course of the disease.

- The therapeutic methods of the invention are, in some cases, targeted to prenatal treatment. For example, a fetus found to have a prostate-specific or testis-specific mutation is administered a gene therapy vector including a normal prostate-specific or testis-specific gene, or administered a normal prostate-specific or testis-specific protein. Such treatment may be required only for a short period of time, or may, in some form, be required throughout such a patient's lifetime. Any continued need for treatment,
- 5 however, is determined using, for example, the diagnostic methods described above. Also as discussed above, prostate-specific or testis-specific polypeptide or nucleic acid molecule abnormalities may be associated with diseases in adults, and thus, adults are subject to the therapeutic methods of the invention as well.
- 10 Additionally, prostate-specific or testis-specific polypeptides may be used to stimulate an immune system to assist in generating immunity against, for example, prostate cancer cells.

- The methods of the present invention can be used to diagnose or treat the disorders described herein in any mammal, for example, humans, domestic pets, or livestock. Where a non-human mammal is treated or diagnosed, the prostate-specific or testis-specific polypeptide, nucleic acid molecule, or antibody employed is preferably specific for that species.
- 20

Identification of Molecules that Modulate Prostate-Specific Or Testis-Specific Polypeptide or Nucleic Acid Molecule Biological Activity or Whose Biological Activity is Modulated by Prostate-Specific Or Testis-Specific Polypeptides or Nucleic Acid Molecules

5 Isolation of prostate-specific or testis-specific cDNAs (as described herein) also facilitates the identification of molecules that increase or decrease prostate-specific or testis-specific polypeptide or nucleic acid molecule biological activity. Similarly, molecules whose activity is modulated by prostate-specific or testis-specific polypeptide or nucleic acid
10 molecule biological activity can be identified. According to one approach, candidate molecules are added at varying concentrations to the culture medium of cells expressing prostate-specific or testis-specific mRNA. Prostate-specific or testis-specific biological activity is then measured using standard techniques. The measurement of biological activity can include,
15 without limitation, the measurement of prostate-specific or testis-specific protein and nucleic acid molecule expression levels, response to androgens, or intracellular localization and trafficking.

If desired, the effect of candidate modulators on expression can also be measured at the level of prostate-specific or testis-specific protein
20 production using the same general approach and standard immunological detection techniques, such as western blotting or immunoprecipitation with a prostate-specific or testis-specific-specific antibody (see below).

A test compound that is screened in the methods described above can be a chemical, be it naturally-occurring or artificially-derived. Such
25 compounds can include, for example, polypeptides, synthesized organic molecules, naturally occurring organic molecules, nucleic acid molecules, and components thereof. Candidate prostate-specific or testis-specific modulators include peptide as well as non-peptide molecules (e.g., peptide

or non-peptide molecules found, *e.g.*, in a cell extract, mammalian serum, or growth medium in which mammalian cells have been cultured).

- 5 Administration of Prostate-Specific Or Testis-Specific Polypeptides,
Prostate-Specific Or Testis-Specific Nucleic Acid Molecules, and
Modulators of Prostate-Specific Or Testis-Specific Polypeptide or Nucleic
Acid Molecule Synthesis or Function

A prostate-specific or testis-specific protein, nucleic acid molecule, or modulator is administered within a pharmaceutically-acceptable diluent, 10 carrier, or excipient, in unit dosage form to patients or experimental animals. Also, conventional pharmaceutical practice is employed to provide suitable formulations or compositions in which to administer neutralizing prostate-specific or testis-specific antibodies or prostate-specific or testis-specific-inhibiting compounds (*e.g.*, a prostate-specific or 15 testis-specific antisense molecule or a prostate-specific or testis-specific dominant negative mutant) to patients suffering from a prostate-specific or testis-specific disease, such as prostate cancer, testicular cancer, benign hyperplasia of the prostate, or developmental defects of the prostate or testis. Administration can begin before or after the patient is symptomatic.

20 Any appropriate route of administration can be employed, for example, administration can be parenteral, intravenous, intra-arterial, subcutaneous, intramuscular, intracranial, intraorbital, ophthalmic, intraventricular, intracapsular, intraspinal, intracisternal, intraperitoneal, intransanal, inhalation to deep lung, aerosol, by suppositories, oral, or topical 25 (*e.g.* by applying an adhesive patch carrying a formulation capable of crossing the dermis and entering the bloodstream). Preferably, the administration is local to the afflicted tissue, such as prostate or testis tissue. Therapeutic formulations can be in the form of liquid solutions or suspensions; for oral administration, formulations can be in the form of

tablets or capsules; and for intranasal formulations, in the form of powders, nasal drops, or aerosols. Any of the above formulations may be a sustained-release formulation.

Methods that are well known in the art for making formulations are 5 found, for example, in *Remington's Pharmaceutical Sciences*, (18th edition), ed. A. Gennaro, 1990, Mack Publishing Company, Easton, PA. Formulations for parenteral administration can, for example, contain excipients; sterile water; or saline; polyalkylene glycols, such as polyethylene glycol; oils of vegetable origin; or hydrogenated naphthalenes. 10 Sustained-release, biocompatible, biodegradable lactide polymer, lactide/glycolide copolymer, or polyoxyethylene-polyoxypropylene copolymers can be used to control the release of the compounds. Other potentially useful parenteral delivery systems for prostate-specific or testis-specific modulatory compounds include ethylene-vinyl acetate copolymer 15 particles, osmotic pumps, implantable infusion systems, and liposomes. Formulations for inhalation can contain excipients, for example, lactose, or can be aqueous solutions containing, for example, polyoxyethylene-9-lauryl ether, glycocholate, and deoxycholate, or can be oily solutions for administration in the form of nasal drops, or as a gel.

20

Prostate-Specific Or Testis-Specific Fragments

Polypeptide fragments that include various portions of prostate-specific or testis-specific proteins are useful in identifying the domains important for their biological activities, such as protein-protein interactions 25 and transcription. Methods for generating such fragments are well known in the art (see, for example, Ausubel *et al.*, *supra*), using the nucleotide sequences provided herein. For example, a prostate-specific or testis-specific protein fragment can be generated by PCR amplifying a desired prostate-specific or testis-specific nucleic acid molecule fragment using

- oligonucleotide primers designed based upon the prostate-specific or testis-specific nucleic acid sequences. Preferably, the oligonucleotide primers include unique restriction enzyme sites that facilitate insertion of the amplified fragment into the cloning site of an expression vector (e.g., a mammalian expression vector, see above). This vector can then be introduced into a cell (e.g., a mammalian cell; see above) by artifice, using any of the various techniques known in the art such as those described herein, resulting in the production of a prostate-specific or testis-specific polypeptide fragment in the cell containing the expression vector.
- 10 Prostate-specific or testis-specific polypeptide fragments (e.g., chimeric fusion proteins) can also be used to raise antibodies specific for various regions of prostate-specific or testis-specific polypeptides. Preferred prostate-specific or testis-specific fragments include, without limitation, fragments including the N-terminal domain of STMP1 (amino acids 1-200), the P5CR domain, and fragments thereof.
- 15

Synthesis of Prostate-Specific Or Testis-Specific Proteins, Polypeptides, and Polypeptide Fragments

Those skilled in the art of molecular biology will understand that a wide variety of expression systems can be used to produce recombinant prostate-specific or testis-specific proteins. The precise host cell used is not critical to the invention. The prostate-specific or testis-specific proteins can be produced in a prokaryotic host (e.g., *E. coli*) or in a eukaryotic host (e.g., *S. cerevisiae*, insect cells such as Sf9 cells, or mammalian cells such as COS, NIH 3T3, CHO, or HeLa cells). These cells are commercially available from, for example, the American Type Culture Collection, Rockville, MD (see also Ausubel *et al.*, *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, NY, 1998). The method of transformation and the choice of expression vehicle (e.g., expression

vector) will depend on the host system selected. Transformation and transfection methods are described, e.g., in Ausubel *et al.*, *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, NY, 1998, and expression vehicles can be chosen from those provided, e.g. in Pouwels *et al.*, *Cloning Vectors: A Laboratory Manual*, 1985, Supp. 1987).

The characteristics of prostate-specific or testis-specific nucleic acid molecules are analyzed by introducing such genes into various cell types or using *in vitro* extracellular systems. The function of prostate-specific or testis-specific proteins produced in such cells or systems are then examined under different physiological conditions. Also, cell lines can be produced that over-express the prostate-specific or testis-specific gene product, allowing purification of prostate-specific or testis-specific proteins for biochemical characterization, large-scale production, antibody production, and patient therapy.

The polypeptides of the invention may be produced *in vivo* or *in vitro*, and may be chemically and/or enzymatically modified. The polypeptides can be isolated from prostate tissue or prostate cancer cells that may or may not be in a hormone dependent state. Alternatively, and especially where larger amounts (*i.e.*, >10mg) are desirable, recombinant production (*e.g.*, in a bacterial, yeast, insect cell, or mammalian cell system) may advantageously be employed to generate significant quantities of prostate-specific or testis-specific polypeptides.

Furthermore, recombinant production not only offers a more economical strategy to produce the polypeptides of the invention, but also allows specific modification in the amino acid sequence and composition to tailor particular biochemical, catalytic and physical properties. For example, where increased solubility is desirable, one or more hydrophobic amino acids may be replaced with hydrophilic amino acids.

Alternatively, where reduced or increased catalytic activity is required, one or more amino acids may be replaced or eliminated.

In still another example, the polypeptides of the invention can be synthesized as fusion proteins including, for example, fusions with enzymatically active partners (e.g., for dye formation or substrate conversion) and fluorescent partners such as GFP, EGFP, BFP, etc.

With respect to chemical and enzymatic modifications of contemplated polypeptides, it is many modifications are appropriate, including addition of mono-, and bifunctional linkers, coupling with protein- and non-protein macromolecules, and glycosylation. For example, mono- and bifunctional linkers are especially advantageous where polypeptides are immobilized to a solid support, or covalently coupled to a molecule that enhances immunogenicity of contemplated polypeptides (e.g., KLH, or BSA conjugation). Alternatively, the polypeptides may be coupled to antibodies or antibody fragments to allow rapid retrieval of the polypeptide from a mixture of molecules. Further couplings include covalent and non-covalent coupling of polypeptides with molecules that prolong the serum half-life and/or reduce immunogenicity such as cyclodextranes and polyethylene glycols.

20

Use of Prostate-Specific Or Testis-Specific Antibodies

Antibodies to prostate-specific or testis-specific proteins are used to detect prostate-specific or testis-specific proteins or to inhibit the biological activities of prostate-specific or testis-specific proteins. For example, a nucleic acid molecule encoding an antibody or portion of an antibody can be expressed within a cell to inhibit prostate-specific or testis-specific function. In addition, the antibodies can be coupled to compounds, such as radionuclides and liposomes for diagnostic or therapeutic uses. Antibodies that inhibit the activity of a prostate-specific or testis-specific polypeptide

can also be useful in preventing or slowing the development of a disease caused by inappropriate expression of a wild type or mutant prostate-specific or testis-specific gene. For example, the antibodies of the invention may be utilized to localize and locally quantify disease-specific 5 markers in prostate or testis tissue sections, e.g., in prostate or testicular cancer.

Detection Of Prostate-Specific Or Testis-Specific Gene Expression

As noted, the antibodies described above can be used to monitor 10 prostate-specific or testis-specific protein expression. *In situ* hybridization of RNA can be used to detect the expression of prostate-specific or testis-specific genes. RNA *in situ* hybridization techniques rely upon the hybridization of a specifically labeled nucleic acid probe to the cellular RNA in individual cells or tissues. Therefore, RNA *in situ* hybridization is 15 a powerful approach for studying tissue- and temporal-specific gene expression. In this method, oligonucleotides, cloned DNA fragments, or antisense RNA transcripts of cloned DNA fragments corresponding to unique portions of prostate-specific or testis-specific genes are used to detect specific mRNA species, e.g., in the tissues of animals, such as mice, 20 at various developmental stages, or to monitor tumor progression. Other gene expression detection techniques are known to those of skill in the art and can be employed for detection of prostate-specific or testis-specific gene expression.

25 Identification of Additional Prostate-Specific Or Testis-Specific Genes

Standard techniques, such as the polymerase chain reaction (PCR) and DNA hybridization, as well as the SSH and other techniques described herein, can be used to clone prostate-specific or testis-specific homologues in other species and other prostate-specific or testis-specific genes in

humans. Prostate-specific or testis-specific genes and homologues can be readily identified using low-stringency DNA hybridization or low-stringency PCR with human prostate-specific or testis-specific probes or primers. Degenerate primers encoding human prostate-specific or testis-specific or human prostate-specific or testis-specific amino acid sequences can be used to clone additional prostate-specific or testis-specific genes and homologues by RT-PCR.

Additional prostate-specific or testis-specific genes include genes expressed during various growth and developmental phases of the diseased prostate or testis, e.g., those involved in prostate cancer, benign prostatic hyperplasia, or testicular cancer, and genes expressed as a result of a drug regimen.

Construction of Transgenic Animals and Knockout Animals

Characterization of prostate-specific or testis-specific genes provides information that allows prostate-specific or testis-specific knockout animal models to be developed by homologous recombination. Preferably, a prostate-specific or testis-specific knockout animal is a mammal, most preferably a mouse. Similarly, animal models of prostate-specific or testis-specific overproduction can be generated by integrating one or more prostate-specific or testis-specific sequences into the genome of an animal, according to standard transgenic techniques. Moreover, the effect of prostate-specific or testis-specific gene mutations (e.g., dominant gene mutations) can be studied using transgenic mice carrying mutated prostate-specific or testis-specific transgenes or by introducing such mutations into the endogenous prostate-specific or testis-specific gene, using standard homologous recombination techniques.

A replacement-type targeting vector, which can be used to create a knockout model, can be constructed using an isogenic genomic clone, for

example, from a mouse strain such as 129/Sv (Stratagene Inc., LaJolla, CA). The targeting vector can be introduced into a suitably-derived line of embryonic stem (ES) cells by electroporation to generate ES cell lines that carry a profoundly truncated form of a prostate-specific or testis-specific gene. To generate chimeric founder mice, the targeted cell lines are injected into a mouse blastula-stage embryo. Heterozygous offspring can be interbred to homozygosity. Prostate-specific or testis-specific knockout mice provide a tool for studying the role of prostate-specific or testis-specific polypeptides and nucleic acid molecules in embryonic development and in disease. Moreover, such mice provide the means, *in vivo*, for testing therapeutic compounds for amelioration of diseases or conditions involving a prostate-specific or testis-specific polypeptide or nucleic acid molecule-dependent or prostate-specific or testis-specific polypeptide or nucleic acid molecule-affected pathway.

15

Animal Models

The prostate-specific and testis-specific polypeptides, antisense compounds, etc., of the invention can also be used in conjunction with animal models of prostate or testis disorders, to test the therapeutic, diagnostic, and screening methods of the invention. An exemplary prostate cancer model in transgenic mice is called TRAMP, in which the SV40 large T antigen is targeted to the prostate (Greenberg et al., PNAS 92, 3439-3443, 1995). Another test system is the CWR22 (androgen-dependent) and CWR22R (androgen-independent) xenografts, as known in the art and as described herein. Growth, PSA secretion, metastasis, etc. of these xenografts could be monitored in the presence and absence of the prostate-specific or testis-specific polypeptides, nucleic acid molecules, and other compounds of the invention. Other animal models, for example, animal

models of other forms of cancer, or immunocompromised animals, e.g., nude mice, may also be used.

The following Examples will assist those skilled in the art to better
5 understand the invention and its principles and advantages. It is intended
that these Examples be illustrative of the invention and not limit the scope
thereof.

10

EXAMPLE 1

Suppression Subtraction Of Prostate- And Testes-Specific Genes And Subcloning Into Pzero

cDNA derived from poly(A)+ RNA of 10 different normal human tissues were subtracted against normal human prostate cDNA using
15 suppression subtraction hybridization (SSH) (Diatchenko, L. et al., *Proc. Natl. Acad. Sci. USA* 93, 6025-6030, 1996) and the resulting cDNA fragments were cloned into an appropriate vector. SSH was performed as described (Clontech PCR-Select Cloning Kit) using prostate poly(A)+ RNA against a pool of poly(A)+ RNA obtained from ten normal human tissues
20 (heart, brain, placenta, lung, liver, skeletal muscle, kidney, spleen, thymus, and ovary). Upon secondary PCR amplification (12 cycles), the reactions were extracted with phenol/chloroform, the DNA with ethanol, and the pellets washed once with 70% ethanol. After drying, the DNA pellet was dissolved in 0.2XTE or MQ dH₂O and cut with RsaI in a 20 µl reaction for
25 2 hrs at 37°C to excise adaptors. After digestion, the reactions were run on a 1.5% agarose gel, with molecular size markers on one side, at 5 V/cm, 40 min. Care was taken not to expose the gel to short wavelength UV light. The adapter bands were excised, and the gel was run at 5 V/cm for 15 min in a reversed electric field to concentrate the cDNA bands.

The gel was visualized (long wave UV light) and the amplified cDNAs, ranging in size between 100 bp-1kB, were excised. The DNA was purified using the QIAEX gel DNA purification kit. The purified DNA was cloned into EcoRV-cut, dephosphorylated pZERO (Invitrogen).

- 5 Ligation reactions were performed in 10 µl final volume in the presence of 5% PEG, 1X T4 Ligase buffer at 37°C overnight and a 1/5 dilution of 1µl of the ligation mix (PSL) was transformed into DH10B electrocompetent cells ($>10^{10}$ efficiency) or equivalent. Colonies were picked and the presence of cDNA inserts was confirmed. To that end, PCR was performed
- 10 with T7 and SP6 primers directly from the colonies. 10% of the reactions were run on a 1.5% agarose gel to visualize amplified products. The colonies with inserts were grown and glycerol stocks (15%) were prepared and stored at -80°C.

15

EXAMPLE 2

Reverse Northern Blot And Sequence Analyses

- To clone androgen-responsive genes represented in the PSL, the reverse northern technique was used (Hedrick, S.M. et al., *Nature* 308, 149-153, 1984; Sakaguchi, N. et al., *EMBO J* 5: 2139-2147, 1986). In this procedure, RNA made from two populations of cells that are to be compared is used to make cDNA probes that are then hybridized to two identical arrays of clones. To that end, PSL clones were amplified by PCR and spotted on nylon filters in 96-well format to generate two identical blots for each set of 92 clones (the remaining four spots were used for positive and negative controls). To make the probes, the androgen-responsive prostate cancer cell line LNCaP was used (Horoszewicz, J.S. et al., *Cancer Res.* 43, 1809-1818, 1983) and was either left untreated (the (-) probe) or treated with the synthetic androgen R1881 for 24 hours (the (+) probe). Poly(A)+ RNA was isolated from these cells and was used to make

the ^{32}P -labeled probes. After hybridization with the (-) and (+) probes, clones that showed differential hybridization were selected for further analysis, i.e., confirmation by a secondary reverse northern blot, and northern blotting.

- 5 Reverse northern screening on the cDNA clones was done essentially as described previously (Hedrick, S.M. et al., *supra*; Sakaguchi, N. et al., *supra*) with some modifications. DNA (approximately 400 ng) from PCR amplification in step 6 was diluted in 200 μl of 0.4M NaOH, 10 mM EDTA and mixed well by pipetting. After incubation at 95°C for 5-10 minutes,
- 10 the tubes were chilled on ice. Denatured DNA was blotted on two separate pieces of Zeta Probe GT+ membrane (Bio-Rad) using a dot-blot apparatus (Bio-Rad). Positive (Prostate specific antigen (PSA) cDNA) and negative (glyceraldehyde 3-phosphate dehydrogenase (G3PDH) cDNA) controls were included on each blot (bottom right) in duplicate. The membranes
- 15 were rinsed with 2XSSC, air dried, and then baked at 80°C for 30 minutes. An exemplary reverse northern analysis is shown in Figure 1. Note that there was a substantial increase in PSA hybridization in the (+) blot (probe prepared from cells that have been stimulated by androgens) compared with the (-) blot (probe prepared from unstimulated cells), whereas there was no significant change in hybridization of G3PDH between the two blots.
- 20 Arrowheads indicate the positive clones identified in this experiment.

25 To verify the tissue-specific nature of the isolated sequences, positive clones were tested in a standard northern blot against RNA preparations of multiple non-prostate tissue samples. Figure 2 shows a multiple tissue northern blot using NKX3A as a probe, to show an exemplary tissue expression pattern seen in the positive clones. Lanes 1-10, and 12-16 are RNA preparations from non-prostate tissues, lane 11 is a RNA preparation from prostate, lane 12 is a RNA preparation from testis.

Twelve clones with no significant homology to known sequences (by BLAST analysis) were isolated from prostate tissue and LNCaP cells. SEQ ID NOS: 1-9 were identified as androgen-responsive differentially-expressed genes in the prostate, while SEQ ID NOS: 10-12 were identified 5 as androgen-responsive differentially-expressed genes in LNCaP cells.

EXAMPLE 3

Isolation And Characterization Of The STMP1 Gene And mRNA

A normal prostate cDNA library was screened by 5'- and 3'-RACE 10 analysis, and resulted in the full-length cDNA for L74. Since computer-aided secondary structure prediction of the deduced amino acid sequence of L74 suggested the presence of a six-transmembrane domain in its C-terminal half, L74 was renamed Six-Transmembrane Protein of Prostate 1 (STMP1).

When the full-length *STMP1* cDNA was used in BLAST analysis, it 15 was found to match a BAC clone (GenBank accession # AC002064) except for a 313 bp repetitive unit in the 3' UTR region, thereby identifying it as the *STMP1* gene and localizing it to Chr7q21. The repetitive region is likely to be a cloning or sequencing artifact of the BAC clone. Computational 20 exon/intron junction analysis and alignment of the full-length cDNA sequence with the BAC clone revealed that *STMP1* gene is composed of six exons and five introns (Figure 4A). The transcription start site, the location and size of the exons and introns, and the location of the partial cDNA clone L74 (black box) are indicated. The start (atg) and stop codons (tga), 25 as well as the putative polyadenylation signal (pA) are also indicated. The first two exons are short, non-coding exons of 83 and 61 bp, whereas exons 3-6 encode the open reading frame (ORF) and are 525, 528, 165, and 3281 bp long, respectively (Figure 4C). The *STMP1* gene spans around 26 kb, which is in part due to the extremely large size of intron 2 (12713 bp).

There are three different predicted promoters within 4 kb upstream of the *STMP1* initiation codon, none of which has any significant TATA or CAAT box consensus sequences, suggesting that *STMP1* is transcribed from a TATA-less promoter.

- 5 The *STMP1* cDNA (GenBank accession # AY008445) has a predicted 5' untranslated region (5'UTR) of approximately 1 kb (deduced by RACE analysis) and an unusually long 3'UTR of approximately 4 kb that comprises ~77% of the total cDNA sequence. The ORF starts within the 3rd exon and is predicted to encode a 490 amino-acid protein (Figure 4B).
- 10 A search for protein motifs identified six predicted transmembrane domains in the C-terminal half of STMP1 starting at F209 (Figures 4B and 4E). Only the cDNA sequence surrounding the ORF is indicated. The exon-intron junctions are indicated and the location of the predicted transmembrane domains are highlighted (TM 1-6) (Figure 4B). The stop codon is indicated with an asterisk. STMP1 has two alternatively spliced forms, shown in Figures 4F-4K, which lead to two predicted isoforms of the protein.
- 15

EXAMPLE 4

- 20 STMP1 Belongs To A New Subfamily Of Six-Transmembrane Domain Proteins

BLAST analysis of GenBank with the predicted STMP1 amino acid sequence identified two independent ESTs and STEAP, a recently discovered cell membrane protein enriched in prostate for expression. An alignment of these sequences, obtained by Clustal and GenDoc programs, is shown in Figure 5. Completely conserved residues are shaded in black; residues that are conserved in two or three of the sequences are shaded light and dark gray, respectively. This alignment suggested that while the EST

BAA91839 cDNA may be close to full-length, BAB15559 cDNA may represent a partial sequence.

The sequences of two proteins related to STMP1 were determined (Figures 4L and 4M, STMP2 and STMP3, respectively). The STMP2 and 5 STMP3 sequences contain the EST sequences. The GFP-fusion of STMP2 gives similar localization as STMP1. Both STMP2 and STMP3 are more widely distributed and have higher levels in some tissues other than the prostate. For example, STMP2 has the highest expression in the placenta and the lung, and is also highly expressed in the heart, liver, prostate, and 10 testis, while STMP3 has the highest expression in the liver, and is also highly expressed in the heart, placenta, lung, kidney, pancreas, prostate, testis, small intestine, and colon.

The sequence similarity between STMP1 and STEAP is limited and not significant before residue 210 of STMP1 where the predicted six- 15 transmembrane coding domain starts. This suggests that the N-terminal region is structurally and functionally related among STMP proteins, forming a six-transmembrane protein subfamily that is distinct from STEAP.

20 EXAMPLE 5

STMP1 Expression Is Highly Enriched In Prostate

The expression profile of *STMP1* was then determined in various human tissues by Northern analysis, in which a multiple tissue Northern blot was hybridized to the *STMP1* probe (see Materials and Methods). As 25 shown in Figure 6A, *STMP1* hybridized to a major mRNA species of 6.5 kb, and three minor mRNA species of 2.2, 4.0, and 4.5 kb in the prostate tissue. The stronger hybridization that is observed with G3PDH in the heart and skeletal muscle samples is due to its higher expression in these tissues. The lanes represent: 1. Heart, 2. Brain, 3. Placenta, 4. Lung, 5.

Liver, 6. Skeletal Muscle, 7. Kidney, 8. Pancreas, 9. Spleen, 10. Thymus, 11. Prostate, 12. Testis, 13. Ovary, 14. Small Intestine, 15. Colon, 16. Peripheral blood leukocyte. The location of the full-length 6.5 kb mRNA, as well as the lower molecular weight *STMP1* species are indicated by 5 arrows to the left of the figure. There was 15-20-fold lower mRNA expression of the 6.5 kb band in the heart, brain, kidney, pancreas, and ovary, compared to prostate, and no detectable expression in other tissues. In contrast, the three lower molecular weight species, encoded by alternatively spliced forms of *STMP1*, were only detectable in the prostate. 10 Hybridization with a glyceraldehyde 3-phosphate dehydrogenase (G3PDH) cDNA probe resulted in approximately similar signals in all lanes, except for the heart and skeletal muscle where G3PDH is known to be more abundant compared with other tissues. These data show that *STMP1* expression is high in the prostate, although expression can be seen in other 15 tissues, and that *STMP1* has isoforms that are restricted to the prostate for expression.

EXAMPLE 6

Characterization Of STMP1 Expression

20 Since androgen is a major hormonal stimulus for the normal prostate gland and for early stage prostate cancer, the possible androgen regulation of *STMP1* was assessed by Northern analysis in the androgen-responsive prostate cancer cell line LNCaP. Cells were either left untreated or treated with the synthetic androgen R1881 (10^{-8} M) with increasing amounts of 25 time (hours) as indicated (Figure 6B), harvested, and total RNA isolated and used in Northern analysis with *STMP1* cDNA as probe. The same membrane was also probed for the androgen-dependent gene PSA. Relative induction of mRNA accumulation is indicated at the bottom of the lanes, as determined by phosphorimager analysis (Molecular Dynamics).

The CWR22 xenograft was grown in nude mice and tumor samples were collected either before ($t=0$) or 1, 2, or 4 weeks after castration. Total RNA was isolated and was then used in Northern analysis with the same probes. Ethidium bromide-stained 18S RNA is shown as a control for RNA integrity and loading. At 6 h, there was an approximately 25% increase in *STMP1* expression, which was lost by 24 h, with a final 20% decrease observed at 48 h compared with basal levels. In contrast, the mRNA accumulation of the androgen-regulated gene PSA dramatically increased upon androgen stimulation in a time-dependent manner, as expected, reaching approximately 22-fold higher levels by 48 hours. Relative induction of *STMP1* mRNA accumulation is indicated at the bottom of the lanes determined by phosphorimager analysis. As is shown in Figure 6B, *STMP1* displayed similar expression levels in untreated and R1881-treated LNCaP cells, indicating that *STMP1* expression is not significantly regulated by androgens in LNCaP cells.

To determine the possible androgenic regulation of *STMP1* expression in an *in vivo* setting, the androgen-dependent xenograft model CWR22, which is derived from a primary human prostate tumor was used (Wainstein, M. A. et al., *Cancer Res* 54, 6049-6052, 1994). Since they are androgen-dependent for growth, the CWR22 tumors in nude mice display marked regression upon castration and may regress completely. CWR22 xenografts were grown in nude mice in the presence of a sustained release testosterone pellet. After the tumors had grown, the mice were castrated, the testosterone pellets were removed, and the regressing tumors were collected at 1, 2, or 4 weeks post-castration. Total RNA was prepared from these tumor samples and used in Northern analysis. As shown in Figure 6B, similar to the observations in LNCaP cells, *STMP1* mRNA accumulation in the CWR22 tumors showed no significant change upon castration and was not affected by the presence of androgens (note that

there is underloading of RNA for CWR22 2wk sample). In contrast, the mRNA accumulation of the androgen-regulated gene PSA was dramatically decreased upon castration, dropping to approximately 16% of pre-castrate levels by two weeks post-castration. These results are consistent with the 5 findings in LNCaP cells and suggest that *STMP1* expression is not significantly regulated by androgens in prostate cancer cells. *STMP1* expression was substantially lower in the CWR22 tumors compared with LNCaP cells.

The expression profile of *STMP1* was also analyzed in the androgen-10 independent prostate cancer cell lines PC3 and DU145, as well as in four independent, relapsed derivatives of CWR22 tumors, named CWR22R (Nagabhusan, M. et al., *Cancer Res* 56, 3042-3046, 1996), representative of advanced prostate cancer (Figure 6C). LNCaP (in the presence (+) or absence (-) of R1881 (10^{-8} M)), PC-3, or DU-145 cells were grown and total RNA was isolated. Four independent lines of the androgen independent human prostate cancer xenograft CWR22R, were grown in nude mice, tumors were collected, and total RNA was isolated and used in Northern analysis with *STMP1* or the androgen target gene *NKX3.1* cDNAs as probes. Ethidium bromide-stained 18S RNA is shown as a control for 15 RNA integrity and loading. The relative induction of *STMP1* and *NKX3.1* mRNA accumulation is indicated at the bottom of the lanes determined by phosphorimager analysis (Molecular Dynamics). As is shown in Figure 6C, *STMP1* expression was high in LNCaP cells and did not significantly change in response to R1881 treatment compared with a ~9-fold induction 20 of the androgen target gene *NKX3.1*. There was no *STMP1* expression in the androgen-independent prostate cancer cell lines PC-3 or DU-145, as was the case for *NKX3.1*. In contrast, there was significant *STMP1* expression in tumors from all four independent CWR22R xenograft lines 25 tested, ranging between ~30-60% of that observed in LNCaP cells. A

similar overexpression pattern was also observed for *NKX3.1* (Figure 6C) consistent with previous findings (Korkmaz, K. S. et al., *Gene* 260, 25-36, 2000).

- An interesting property of *STMP1* expression profile is that even though it is expressed at low levels in the androgen dependent CWR22 xenograft, it is highly expressed in the relapsed CWR22R which is androgen receptor (AR) positive, but is not responsive to androgens. This indicates that *STMP1* expression is deregulated once the prostate tumor progresses from an androgen-dependent to an androgen-independent phase.
- In addition, *STMP1* is not expressed in the AR-negative prostate cancer cell lines PC-3 and DU-145, but is expressed at high levels in the AR-positive cell line LNCaP and the CWR22 and CWR22R xenografts. Thus, expression of *STMP1* is correlated with the presence of a functional AR in the cell.
- It has been known for over 50 years that androgens play a key role both in the development and maintenance of the normal prostate and the initiation and progression of prostate cancer. Androgen withdrawal results in involution of both the normal prostate gland as well as a prostate tumor in the early stages of the disease that is still androgen dependent.
- Consequently, androgen withdrawal is commonly used as treatment to reverse tumor growth. However, in the case of the prostate tumor, after a few months or years, the tumor recurs in almost all cases in an androgen-independent state. At this point there is no effective therapy and prognosis for survival is extremely poor. Since *STMP1* is overexpressed during this later androgen-insensitive state, it will be a useful tool in diagnostic and therapeutic applications for prostate cancer.

These data indicate that *STMP1* expression is deregulated once prostate cancer progresses from an androgen-dependent to an androgen-independent state.

EXAMPLE 7Intracellular Localization Of STMP1

To gain insight into the intracellular localization pattern of *STMP1*, a
5 green fluorescent protein (GFP)-STMP1 fusion protein was generated. The
use of such GFP chimeric proteins has recently become a standard method
to assess intracellular localization and dynamics of proteins. COS-1 cells
were transiently transfected with GFP-STMP1, fixed and processed for
confocal microscopy as described in Materials and Methods.

10 A series of 11 confocal sections along the z-axis were collected
through a single cell at nominal 100 nm intervals. Three of the consecutive
sections and the projection of all 11 sections are shown in Figure 7A.
Arrows indicate tubular-vesicular structures (VTS) in different sizes,
shapes, and locations (Bar=5 μ m). In all 11 z-plane sections, GFP-STMP1
15 showed bright juxtanuclear distribution pattern, characteristic of the Golgi
complex. Additionally, GFP-STMP1 was dispersed in spots of variable size
throughout the cytoplasm and at the cell periphery (z-7, projection). Some
of these bright fluorescent spots were tubular (z-6, arrow and Figure 8) or
vesicular (z-5, arrow) in morphology.

20 To determine more directly whether GFP-STMP1 was localized to
the Golgi complex, we compared its intracellular distribution with those of
two well characterized Golgi markers, the medial Golgi enzyme
mannosidase II (ManII) (Rabouille, C. et al., *J Cell Sci* 108, 1617-1627,
1995) and the coat protein β -COP (Pepperkok, R. et al., *Cell* 74, 71-82,
25 1993). COS-1 cells were transfected with GFP-STMP1, fixed, labeled with
the appropriate primary and secondary antibodies and imaged by confocal
laser scanning microscopy. Green GFP-STMP1 fluorescence and red
(Texas Red-labeled secondary antisera) β -COP and ManII fluorescence
were detected by confocal laser microscopy. Panels to the right show the

overlay images with yellow/orange staining indicating the regions of colocalization. Bars=5 μ m. As shown in Figure 7B, the distribution of GFP-STMP1 extended throughout the Golgi complex, as evidenced by significant colocalization with both ManII and β -COP. However, some 5 areas of non-overlap between the GFP-STMP1 and both Golgi markers were observed suggesting that STMP1, at least in part, is differentially localized within the Golgi complex compared with these two markers.

Since GFP-STMP1 was associated with VTS (Figure 7A and Figure 8), more specific localization of GFP-STMP1 to the trans-Golgi network 10 (TGN), an important site for the sorting of proteins destined to the plasma membrane, secretory vesicles, or lysosomes (Farquhar, M. G. & Palade, G. E. *Trends Cell Biol* 8, 2-10, 1998; Mellman, I. & Warren, G., *Cell* 100, 99-112, 2000; Lemmon, S. K. & Traub, L. M., *Curr Opin Cell Biol* 12, 457-466, 2000) was assessed. An antibody against TGN46, a TGN resident protein that shuttles between the TGN and the plasma membrane (Prescott AR, et al., *Eur J Cell Biol* 72, 238-246, 1997; Ponnambalam, S. et al., *J Cell Sci.* 109, 675-685, 1996), was used in immunofluorescence 15 microscopy experiments as above. As shown in Figure 7B, GFP-STMP1 extensively colocalized with TGN46, greater than that observed with ManII and β -COP, suggesting that in the Golgi complex, STMP1 is primarily 20 localized to the TGN. Note that the images with TGN46 were obtained with lower objective power.

EXAMPLE 8

25 STMP1 Shuttles Between The Golgi And The Plasma Membrane And Colocalizes To The Early Endosomes

The dynamic properties and intracellular trafficking of GFP-STMP1 were studied using confocal time-lapse imaging in living cells. COS-1 cells were transiently transfected with GFP-STMP1 and, 16 h after transfection,

12 consecutive images were collected from live cells every 20s at 37°C by confocal laser scanning microscope (Figure 8). The upper panel shows a VTS extending out and retracting back to the Golgi body (white arrows). In the middle panel and the first image in the lower panel (160s), red 5 arrows indicate the translocation of a VTS from the Golgi body to the cell periphery. In the lower panel, yellow arrows point to the movement of a VTS from the edge of the cell towards the Golgi body. Note that the results shown are representative of multiple time-lapse analyses and the changes in the images are not due to movement from the plain of focus. Bar=5μm.

10 As shown in Figure 8, some VTS were found to be detaching and some to be associating with the Golgi complex. The VTS were highly dynamic and pleiomorphic in size. Some of the VTS followed straight or curvilinear paths, some moved in a stop-and-go fashion, and some showed saltatory movements. The VTS indicated at the top panel (white arrows) extended 15 away from and then retracted back to the Golgi. The VTS in the middle panel and the first image in the lower panel (red arrows) detached from the Golgi complex, paused, and then moved towards the cell periphery until it disappeared at the cell edge suggesting that STMP1 is associated with the secretory pathway. The VTS in the lower panel (yellow arrow) moved 20 from the cell periphery towards the Golgi body suggesting that STMP1 is localized to the endocytic pathway.

EXAMPLE 9

Colocalization Of GFP-STMP1 With The Early Endosomal Marker EEA1

25 To probe whether GFP-STMP1 was associated with the endocytic pathway, the intracellular distribution of GFP-STMP1 was compared with that of the early endosome protein EEA1 (Stenmark, H. et al., *J Biol Chem* 271, 204048-204054, 1996). COS-1 cells were transfected with GFP-STMP1, fixed, immunostained with EEA1 antibodies and observed by

confocal laser scanning microscopy. Green GFP-STMP1 fluorescence and red (Texas Red-labeled secondary antiserum) EEA1 fluorescence were detected by confocal laser microscopy. The panel to the right shows the overlay images with yellow/orange staining indicating the regions of colocalization. Arrows indicate examples of the VTS in the cell periphery which contain both EEA1 and STMP1. Bar=5 μ m. As shown in Figure 9, EEA1 manifested a similar intracellular distribution in both transfected and untransfected cells. Furthermore, GFP-STMP1 significantly colocalized with EEA1 both in the cell periphery and also in the perinuclear area (Figure 9, arrows) suggesting that STMP1 is associated with early endosomes and the endocytic pathway.

EXAMPLE 10

Isolation And Characterization of the SSH9 Gene And mRNA

The *SSH9* gene was identified and mapped (Figure 10). The predicted promoter site, the transcription start site, and the location and size of the exons and introns are indicated. The start and stop codons, as well as two polyadenylation signals, leading to two alternatively spliced transcripts, are also indicated. Figures 11A-C show the nucleotide and predicted amino acid sequence of *SSH9*, as well as the predicted promoter sequence and exon-intron boundaries.

The expression profile of *SSH9*, determined in various human tissues by Northern analysis (Figure 12C), revealed that the 0.7 kb splice variant of *SSH9* was highly testis-specific, while the 1.4 kb transcript was expressed in both prostate and testis.

The androgen regulation of *SSH9* was examined in LNCaP cells and in CWR22 xenografts (Figure 12A) revealed that *SSH9* is not regulated in LNCaP cells, but is regulated in CWR22 xenografts. The expression

profile of *SSH9* was also examined in the androgen-independent prostate cancer cell lines PC3 and DU145, and in CWR22R cells (Figure 12B).

EXAMPLE 11

5 Isolation And Characterization of the *PSL22* Gene And mRNA

The *PSL22* gene was identified and mapped (Figure 13). The location and size of the exons and introns, the location of the partial cDNA clone (black box), as well as the alignment of the full-length cDNA clone with GenBank Accession Nos. AC008551 and AC011449, are indicated.

10 Figures 14A-C show the nucleotide sequence of the ORF, cDNA and predicted amino acid sequence, as well as the predicted promoter, exon, and UTR sequences of *PSL22*.

15 BLAST analysis of GenBank with the predicted *PSL22* amino acid sequence identified *PSL22* as a Rho binding protein. Figure 15 shows a multiple sequence alignment of *PSL22* with related proteins. Completely conserved residues are shown in black; residues found in three sequences are shaded.

20 The expression profile of *PSL22*, determined in various human tissues by Northern analysis (Figure 116B), revealed that while the highest expression was seen in the prostate, high expression was seen in the kidney, pancreas, and colon.

25 The androgen regulation of *PSL22* was examined in LNCaP cells, in the androgen-independent prostate cancer cell lines PC3 and DU145, and in CWR22R cells (Figure 16A). The results showed that *PSL22* is androgen regulated in LNCaP cells, where it is highly expressed, but is not androgen regulated in the PC3 and DU145 cells.

EXAMPLE 12Materials And Methods

The following materials and methods were used in performing the exemplary experiments shown herein. It is understood that these materials
5 and methods are subject to modifications that do not change the nature of the invention, as will be understood by those of ordinary skill in the art.

Probes

Poly (A)+ RNA 1 µg [(-) or (+)]
10 Random primer (N7) 200 ng

RNAse-free sterile H₂O to 20 ul

Heat at 70°C for 10 min, and chill on ice.

While heating the RNA samples, the following solution was prepared:

15 5X 1st strand buffer 10 µl

0.1 mM DTT 5 µl

10 mM each dTTP+dGTP 2 µl

³²P alpha dATP 5 µl

³²P alpha dCTP 5 µl

20 Superscript II (200 U /µl, BRL) 2µl

The solution was mixed by pipetting, spun briefly, incubated at 25°C for 5 min, and then for an additional 1 hour at 37°C. 2 µl of 10mM dCTP + dATP was added and the mixture was incubated for 30 min at 37°C and then heat inactivated at 70°C for 10 min. Unincorporated nucleotides were
25 removed using prespun G25 columns (Bio-Rad). Specific activity (which should be over 5x10⁸cpm/µg) was calculated.

Hybridization

Freshly prepared 25 ml Hybridization mix (7% SDS, 0.5 M NaHPO₄, 1mM EDTA) was pre-warmed at 65°C and 12.5 ml was used for prehybridization of each membrane, 5-10 min at 65 °C. The probe was
5 heat denatured at 95°C for 3-5 min and transferred to the prehybridization mix at 65°C. Hybridization was carried out at 65°C overnight.

Washing

Wash solution I (2xSSC and 1% SDS) and II (0.1xSSC and 0.5% SDS) were prewarmed, and the membrane were washed once with Solution 10 I and then with Solution II for 30 min at 65°C. The membranes were covered with plastic wrap and exposed to a phosphorimager screen.

Selection

15 Clones that showed differences between the (-) and (+) blots were picked (usually 1-8 on each blot pair). A secondary round of reverse northern analysis for confirmation was performed, this time spotting each clone in duplicate on each blot. After phosphorimager analysis, the blots were stripped in 0.1xSSC and 0.5% SDS for 2x15 min at 95°C and
20 hybridized with a PSA probe (or depending on the hormone that is being used, with a probe for any abundant target genes in the tissue under study). For the clones that were confirmed to be different from PSA, for differential expression in the secondary reverse northern, northern analysis was performed using established protocols. A time course of R1881
25 induction of LNCaP cells, as well as the CWR22 xenograft model upon androgen ablation (Wainstein, M. A. et al., *Cancer Res.* 54, 6049-6052, 1994) and the androgen-independent CWR22R relapsed xenograft (Nagabhan, M. et al., *Cancer Res.* 56, 3042-6, 1996), was used.

Sequence analysis

Sequence analysis was performed by the dideoxy chain termination methods using an ABI automated sequencer. Homology search was done using a basic BLAST algorithm. Figure 3 shows a table of results obtained 5 from the BLAST analysis of isolated clones and their homology to known genes (The cutoff for significant homology was 50% identity).

Isolation of prostate cancer related genes from LNCaP cells

The prostate cancer cell line LNCaP was cultured in two batches in 10 culture conditions similar to those previously described (Horoszewicz JS et al., *Cancer Res.* 43: 1809-1818, 1983). The first batch was left untreated, while the second batch was treated with the synthetic androgen R1881 for 24 hrs. Cells from both batches were harvested and total RNA was then isolated from each batch. From the total RNA, polyA⁺ RNA was obtained 15 using standard procedures, and was used in the Suppression Subtraction Hybridization (SSH; Diatchenko et al., *supra*) procedure to identify hormone regulated genes. The tester in the SSH procedure was cDNA from untreated cells and the driver was cDNA from R1881-treated cells. The suppression subtraction protocol was performed according to the original 20 description of the method (Diatchenko et al., *supra*).

Cell culture

LNCaP, PC-3 and DU-145 cells were routinely maintained and treated as described previously (Korkmaz, K. S. et al., *DNA Cell Biol* 19, 25 499-506, 2000; Korkmaz, K. S. et al., *Gene* 260, 25-36, 2000).

Xenograft studies

Transplantation, growth, and harvesting of tumors from mice bearing the CWR22 and CWR22R xenografts were as previously described (Wainstein, M. A., *supra*; Nagabhushan, M., *supra*).

5

Cloning and plasmid construction

- A 262 bp cDNA fragment was originally obtained from a screen of a prostate specific library (Ausubel, F. M., et al. (1997) *Current Protocols in Molecular Biology* (John Wiley and Sons, New York) and termed L74. 5'
- 10 Rapid Amplification of cDNA Ends (RACE) was performed (oligonucleotide sequences available upon request) using the Marathon-Ready cDNA that was prepared from normal prostate tissue (Clontech) and/or SMART-RACE LNCaP cDNA library (Clontech) that was generated according to the manufacturer's recommendations. RACE
- 15 products were cloned into pCRII-TOPO (Invitrogen), positive clones were confirmed by Southern analysis, and sequenced. In parallel, a λgt10 cDNA library made from a pool of normal human prostates (Clontech) was screened by established procedures to obtain additional clones. Overlapping clones were used to deduce the full-length *STMP1* cDNA sequence.
- 20 The full-length *STMP1* ORF was amplified by using primers centered around the start and stop codons (sequences available upon request) and fused in frame to the C-terminus of green fluorescent protein (GFP) using the vector pcDNA3.1-NT-GFP-TOPO (Invitrogen) to generate GFP-STMP1.
- 25

Northern analysis

Total RNA was prepared by the single step guanidine thiocyanate procedure and used in Northern analysis (18). 15 µg of total RNA was used per lane. Probes were generated by random priming and had a specific

activity of $>3 \times 10^8$ dpm/ μ g. A cDNA fragment of *STMP1* spanning residues 145-2202 bp was used as probe. Bands were visualized and quantitated by phosphorimager analysis (Molecular Dynamics).

5 Confocal microscopy

COS-1 cells were transiently transfected by electroporation using a BTX square-wave pulser at 150 V, 1 ms duration. Cells were grown either on cover slips placed in 6-well tissue culture plates for indirect immunofluorescence or on Lab-Tek Chambered Coverglass (Nalge Nunc International) for live-cell microscopy. Transiently transfected cells were observed 16 h after transfection by Leica TCS-SP confocal microscope. All live-cell experiments were done at 37°C.

Indirect immunofluorescence

15 The indirect immunofluorescence was carried out as previously described (Misteli, T. & Spector, D. L. *Mol Cell* 3, 697-705, 1999). The following antibodies were used: anti- β -coat protein (β -COP) antiserum (kindly provided by J. Lippincott-Schwartz), anti-mannosidase II (kindly provided by T. Misteli), anti-TGN46 (Serotec, kindly provided by J.S. Bonifacino), and anti-EEA1 (Affinity Biotechnologies). Texas Red-conjugated secondary antibodies specific for mouse and rabbit were purchased from ICN Biomedicals (Costa Mesa, CA).

Other Embodiments

25 All publications and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each independent publication or patent application was specifically and individually indicated to be incorporated by reference.

While the invention has been described in connection with specific embodiments thereof, it will be understood that it is capable of further modifications and this application is intended to cover any variations, uses, or adaptations of the invention following, in general, the principles of the invention and including such departures from the present disclosure that come within known or customary practice within the art to which the invention pertains and may be applied to the essential features hereinbefore set forth, and follow in the scope of the appended claims.

CLAIMS

1. A substantially pure prostate-specific or testis-specific polypeptide,
5 said polypeptide sequence comprising a sequence substantially identical to
the sequence of any of SEQ ID NOS: 14, 29, 32, 34, 36, 41, or 53.
2. The substantially pure prostate-specific or testis-specific polypeptide
of claim 1, said polypeptide sequence comprising the sequence of any of
10 SEQ ID NOS: 14, 29, 32, 34, 36, 41, or 53.
3. An isolated nucleic acid molecule encoding a polypeptide of claim 1.
4. The isolated nucleic acid of claim 3, wherein said nucleic acid
15 molecule comprises the sequence of any of SEQ ID NOS: 23, 28, 31, 33,
35, 40, or 52.
5. An isolated prostate-specific or testis-specific nucleic acid molecule,
said nucleic acid molecule comprising a sequence substantially identical to
20 SEQ ID NOS: 1-12, 22, 27, 30, and 51.
6. An isolated prostate-specific or testis-specific nucleic acid molecule,
said nucleic acid molecule consisting essentially of SEQ ID NOS: 15-21,
24-26, 42-50, and 54-70.
25
7. The polypeptide of claim 1, wherein said polypeptide is derived
from a mammal.
8. The polypeptide of claim 6, wherein said mammal is a human.

9. A vector comprising the isolated nucleic acid molecule of claim 3, 5, or 6.
- 5 10. A cell comprising the isolated nucleic acid molecule of claim 3, 5, or 6.
11. A cell comprising the vector of claim 9.
- 10 12. A non-human transgenic animal comprising the isolated nucleic acid molecule of claim 3, 5, or 6.
13. An isolated nucleic acid molecule that hybridizes under high stringency conditions to the complement of any of the sequences set forth
15 in SEQ ID NOS: 1-12, 15-28, 30, 31, 33, 35, 40, 42-50, 51, 52, or 54-70,
wherein said isolated nucleic acid molecule encodes a prostate-specific or testis-specific polypeptide.
14. An isolated nucleic acid molecule, wherein said nucleic acid
20 molecule comprises a sequence that is antisense to the coding strand of any of the prostate-specific or testis-specific nucleic acid molecules set forth in SEQ ID NOS: 1-12, 15-28, 30, 31, 33, 35, 40, 42-50, 51, 52, or 54-70, or a fragment thereof.

15. A probe for analyzing a prostate-specific or testis-specific gene or homolog or fragment thereof, said probe having greater than 55% nucleotide sequence identity to a sequence encoding any of SEQ ID NOS: 1-12, 15-28, 30, 31, 33, 35, 40, 42-50, 51, 52, or 54-70, or fragment thereof,
5 wherein said fragment comprises at least six amino acids, and said probe hybridizes under high stringency conditions to at least a portion of a prostate-specific or testis-specific nucleic acid molecule.
16. The probe of claim 14, wherein said probe has 100% complementarity to a nucleic acid molecule encoding any of SEQ ID NOS: 1-12, 15-28, 30, 31, 33, 35, 40, 42-50, 51, 52, or 54-70, or fragment thereof,
10 wherein said fragment comprises at least six amino acids, and said probe hybridizes under high stringency conditions to at least a portion of a prostate-specific or testis-specific nucleic acid molecule.
- 15 17. An antibody that specifically binds to a prostate-specific or testis-specific polypeptide, said polypeptide comprising an amino acid sequence that is substantially identical to the amino acid sequence of any of SEQ ID NOS: 14, 29, 32, 34, 36, 41, or 53.
- 20 18. A method of detecting a prostate-specific or testis-specific gene or fragment thereof in a cell, said method comprising
contacting the nucleic acid molecule of any of SEQ ID NOS: 1-12,
15-28, 30, 31, 33, 35, 40, 42-50, 51, 52, or 54-70, or a fragment thereof,
25 wherein said fragment is greater than about 18 nucleotides in length, with a preparation of genomic DNA from said cell, under high stringency hybridization conditions, and

detecting DNA sequences having about 55% or greater nucleotide sequence identity to any of SEQ ID NOS: 1-12, 15-28, 30, 31, 33, 35, 40, 42-50, 51, 52, or 54-70, thereby identifying a prostate-specific or testis-specific gene or fragment thereof.

5

19. A method for identifying a test compound that modulates the expression or activity of a prostate-specific or testis-specific polypeptide, said method comprising

contacting said prostate-specific or testis-specific polypeptide with
10 said test compound, and

determining the effect of said test compound on said prostate-specific or testis-specific polypeptide expression or activity.

20. A method of treating a mammal having a disorder of the prostate or
15 testis, said method comprising

administering to said mammal a therapeutically effective amount of a compound that modulates the activity or expression of a prostate-specific or testis-specific polypeptide,

wherein said compound has a beneficial effect on said disorder in
20 said mammal.

21. The method of claim 20, wherein said disorder is prostate cancer.

22. A pharmaceutical composition comprising at least one dose of a
25 therapeutically effective amount of a prostate-specific or testis-specific polypeptide or fragment thereof, in a pharmaceutically acceptable carrier, said composition being formulated for the treatment of a disorder of the prostate or testis.

23. The method of claim 20, wherein the prostate-specific or testis-specific polypeptide comprises an amino acid sequence substantially identical to the amino acid sequence of SEQ ID NOS: 14, 29, 32, 34, 36, 38, 39, 41, 53, or 71-73 and fragments and analogs thereof.

5

24. The method of claim 20, wherein said mammal is a human.

25. A kit for the analysis of a prostate-specific or testis-specific nucleic acid molecule, said kit comprising a nucleic acid molecule probe for
10 analyzing a prostate-specific or testis-specific nucleic acid molecule present in a test subject.

26. A kit for the analysis of a prostate-specific or testis-specific polypeptide, said kit comprising an antibody for analyzing a prostate-specific or testis-specific polypeptide present in a test subject.
15

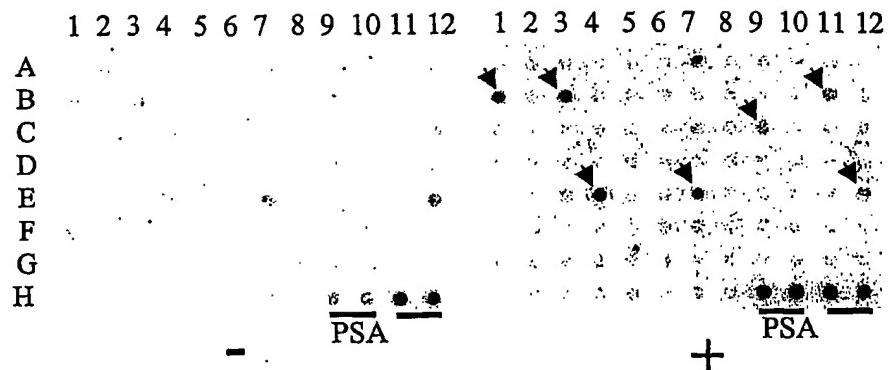
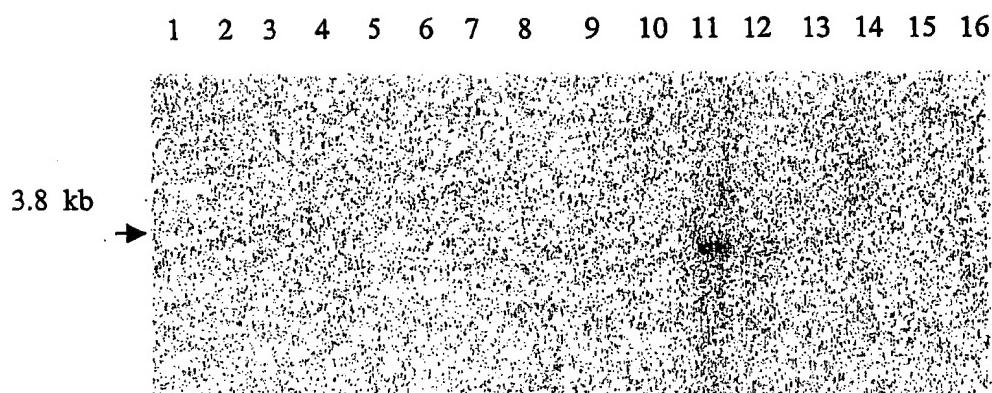


Figure 1



Multiple tissue northern blot. Lane 11: Prostate, 12:testis

Figure 2

SEQ. ID NO.	SEQ. NAME	LENGTH	SEQUENCE
1	PSL 22	251	ACTAATGTGAGGAaCAAACATGTTCAGGCCTGAACATTTCCGGTGCTGACT CGGCcTTAACGTTGTGCCATAATGGAAAATATCTATCTATCTTCTCAA ATCCTGTCTTCATAGTGAAACTCACATTGATGTGTTTATGAAGGAA AGTAACCAAGAAACCTCTAGGAATTAGGAAAAAaGAACCTTTGAGGTG TGTTACTATCTGCTGAAGTTATTTATATAAAGTATTGTAATAGAAaT AGTGTGAGATATGAAATATGGCTATTTAATGGTACAATTATAGACTTT TAGgTCACTATTAATTGGGTACCTATATCcAGT
2	PSL 229A	349	ACACATCCATCATTGTGAAATCTCTTCCAACAAACGTCCTCTTAATGAGC ACAATTCAAAAATCTTGGGACTAAGCTACGAACAAAGTCAACTAAC TACCTACTGACTTCAAAGGAACATATAACCACCGTGTGGTAGCTCATG ACTGTAATCCCAGCACTTGGGAGGCTGAGGCAGGAGGATCACCTGAGCCC AGGAGTCCAGACCAGCCTAAGCAACATGCCAACGACCTGTATGT
3	PSL E15C	51	ACAAAGACACCCCTGYCCCCGGCAAGGTCCCTCAGCTACAAGGGGCCA
4	PSL E156	148	CCXYACATTGTCACAGAGAGGCTCAGGCTTAAAGTTGACCTGCGTAGAAA GCAAGAATGAATTGTTGGAGGAAGTAAGGAGGGCATTGAATAAAGACTTT TAGCAGCTGGGCCAGCTGAACCATCCAAACCCCTTCAAATCCCCTTGT
5	PSL E157	261	ACCCCTAAGTAACCCATTTCAGCCACTCAGATTGATAGGGTGAAAAGACA GGGCAGGTGGTAGCAGCTGTGAAGAAAAGAGGAAGCAGAACGGGTGGCT ATAATCTACAGGCATGTAGAGAGGACTACATAGGCCCTGTCTTGCCTC AGGAGCCCCCTTCTGTCTTGGACTCAGAAATGGATCCTCCAGCACACAT GGCCCAACACTGAGAGTGCAGGAAGCATGGTAGGGCCCTCTGCTGCTGG TATGT
6	PSL E391	121	AGTNTNGGGGANITGAGGGCNGNTAGNNAAANGNTGGNCTACTNTAGA TGCTGCTGAGCGGCCAGTGTGATGGATAACAAGCTTCTTTTTTTT ATTTCGNNTTTTTTTC
7	PSL K31	93	ACTCACTAGGGACTGAGCACTAAATGCTTATTTAAAAGAAATGTAAGAG CAGAAAGCAATTAGGCTACCCCTGCCCTTGTGCTGGCTAGT
8	PSL L28	169	ACACTAAAATAGTTAATGTGATACATTATGTTACATGTATTGCCCAC TGAAAAAATAAAAATATAAACACACAGCAAATGATGACCAGGCCTTGA AGAAAGCTTATAAAAACAAAATAAGAAGCCTGGTACAGAGCGAGACTCTG TCTCAAAAAAAAAA
9	PSL L74	262	ACTTTACAAGCATGAAGGATATTAGGGTAAGTGGCTAATTATAAATCTACT CTAGAGACATATAATCATACAGATTATTCTATAAAATTTCTAGTGTCTCT TCCACATTAAATTGCTATTGCTCAAAGTGTAGAATGCCCTACATTCCCCC ACCCCAAATTGCTATTCTTATTAAAATAGAAAATTATAGGCAAGATACAA TTATATGCGTCTCTTCTGAAATTATAACATTCTAAACTACCCACGTAG GT
10	PSL SSH 20	175	ACAGGTGGCCCTCACCTAGTTGACTCAGCCCTCGATAGTCTAGAGCCCAC CCCCTCCTCAGGAACCTCAAGAGCTCAGCATTATAATGAGCAGTTGGTAAT GAGTTGCCCTATGTGCTTGTGCAAGCAGTCACAGAGATGAGCCCTATTACT TGATATTAGGAACAAAGGT
11	PSL SSH 4	331	ACATCCAAGCCTTCTCGCTGAGAGCAAAGGCTTGTCTACAGCCAGCC AGTCTTGTACTATCTGGCTACTTTAAGGTTAAAAAATAAAAGGCAGTTT CTTTGCTCTGCAGGGCAAGGCAGGAGGGCAGGCCCTCTCATTTGTTCAC ATGTCAAGGAGGAGGAGGCTGTGAGCAAAGGCCACTGGCAAGTTAGGGCAAC ACCAAAGAAGGCTCTGGAGAGACTCCCTGTGGGTGGGGsCTGGCAGGA ACGGTGC:TGTGGACTGTTATGGTCTGTCAGTTGAGGCTTGTGAAACCCCA AGTAAAGTGTAAAAACCTCACT
12	PSL SSH 9	170	ACGACTCATCCACCTCCGGCTGAAGCTCCAGGAGCTGAAGGACCCCAATGA GGATGAGCAAACATCCGAGTGCTCTTGAGCACCCGTTTACAAGGAGAA GAGCAAGAGCGTCAAGCAGACCTGTGACAAGTGTAAACACCATCATCTGGGG GCTCATTAGACCTGGT

Figure 3

STMP1 gene structure

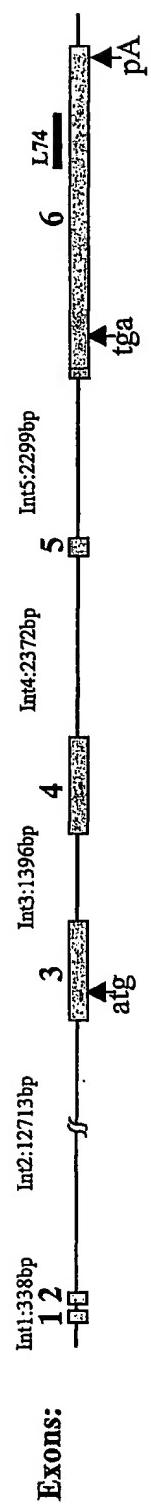


Figure 4A

Figure 4B

EXON_1 83bp

1 ACGCGGGGATCCAGCTGGTAGGCAGGAAGCAGCTGGAGTGCACCGCTACGGCAGC
61 CACCTGCAACGCCAGTCGGAG

EXON_2 61bp

1 AGCTAAGGGCAAGTCCTGAGGTTGGGCCAGGAGAAAGAAGGCAAGGAGACATTGTCCA
61 G

EXON_3 525bp

1 GATATTCTGGTATCTGGAAAGTGTCCGTATCATGGAATCAATCTCTATGATGGGAAGC
61 CCTAAGAGCCTTAGTGAAACTTTTACCTAATGGCATAAATGGTATCAAAGATGCAAGG
121 AAGGTCACTGTAGGTGTGATGGAAGTGGAGATTTGCCAACCTTGACCATTGACTT
181 ATTAGATGCGGCTATCATGGTCATAGGAAGTAGAAATCTAAGTTGCTCTGAATT
241 TTCCCTCATGTGGTAGATGTCACTCATCATGAAGATGCTCTCACAAAAACAAATATAATA
301 TTGTTGCTATACACAGAGAACATTATACCTCCCTGTGGACCTGAGACATCTGCTTGT
361 GGTAAAATCCTGATTGATGTGAGCAATAACATGAGGATAAACAGTACCCAGAATCCAAT
421 GCTGAATATTTGGCTTCATTATCCCAGATTCTTGATTGTCAAGGATTAAATGTTGT
481 TCAGCTGGGCACTTCAGTTAGGACCTAAGGATGCCAGCCGGCAG

EXON_4 528bp

1 GTTTATATATGCAGCAACAATATTCAAGCGCAGAACAGGTTATTGAACTTGCCCCCAG
61 TTGAATTCAITCCCATTGACTTGGATCCTTATCATCAGCCAGAGAGATTGAAAATT
121 CCCCTACGACTCTTACTCTCTGGAGAGGGCCAGTGGTAGTATAAGCTTGGCCACA
181 TTTTTTTCTTTATTCCTTGTCAAGAGATGTGATTCCATATGCTAGAAACCAACAG
241 AGTGACTTTACAAAATTCCTATAGAGATTGTGAATAAAACCTACCTATAGTTGCCATT
301 ACTTGCCTCCCTAGTACACCTCGCAGGTCTCTGGCAGCTGCTTATCAACTTTATTAC
361 GGCACCAAGTATAGGAGATTCCACCTGGTTGGAACCTGGTACAGTGTAGAAAACAG
421 CTTGGATTACTAAGTTTTCTTCGCTATGGTCCATGGTGCCTACAGCCTCTGCTTACCG
481 ATGAGAAGGTCAGAGAGATAATTGTTCTCAATGGTTATCAGCAG

EXON_5 165bp

1 GTTCATGCAAATATTGAAAACCTGGAAATGAGGAAGAAGTTGGAGAATTGAAATGTAT
61 ATCTCCTTGGCATAATGAGCCTGGCTTACCTTCCTCTGGCAGTCACCTCTATCCCT
121 TCAGTGAGCAATGCTTAAACTGGAGAGAATTCAAGTTTATTCAAG

EXON_6 148bp

1 TCTACACTGGATATGCGCTCTGCTCATAGTACTTCCATGTTTAATTATGGATGG
61 AAACGAGCTTTGAGGAAGAGTACTACAGATTATACACCACAAACTTGTCTTGC
121 CTTGTTTGCCCTCAATTGTAATTCTGG

cont_6+UTR

1 GTAAGATTATTATTCTTCCATGTATAAGCCGAAAGCTAAACGAATTAAAAAGGCT
61 GGGAAAAGAGCCAATTCTGAAGAAGGTATTGGAGGAACAACTCCTCATGTCCTCCCG
121 AGAGGGTCACAGTAATGTGATGATAAATGGTTACAGCTGCATATAAAGTTCTACTC
181 ATGCCATTATTATTATGACTTCTACGTTCAAGTATGCTGTCAAATTATCGTGG
241 TTGAAACTTGTAAATGAGATTCAACTGACTTAGTGATAGAGTTCTCAAGTTAAATT
301 TTCACAAATGTCATGTTGCAATATGAATTCTTAGTCACATATTATTGTAATTAG
361 GTATGTTTGTTGTTGACAACGTGAAACCTGTTGTTACTTTATATTCTACAATCA
421 GACAAAAATACAGTTAAATAATAGATATAATGTTAAAACAATTGCAAACCAAGC
481 AGAATTTTAAGCTTTAAAATAATTCAATGGATATAACATTCTGAAGATTAAAGATT
541 TTAATTATTCAACTAAAAAGTAGAAATGCATTATTATACATTCTTAAGAAAGGACAC
601 GTTATGTTAGCATCTAGGTAGGCTGCATGATAGCACTCCTATATTCTCTCATAAAATA
661 GGATTGAGGATGAAATTAAATTGTTGAGCAACATGTTGATTATGAAAGAGACACAAATT
721 AAAAGACAAATTAAACCTGAAATTATAATTAAATATTGAGACATGAAATAACATAC
781 TGATAATTACACCTCATGAAAGATTTATTCTTTATTGTTACAGAGCAGTTCTCATTT
841 TCATATTAAATACTGATCAGGAAGAGGATTCACTGAAACATTGCTCCAAAACGTGCTAT
901 CTCTAATACGGTACCACTCTAGGAACGTACTGATACTAGTTCTACTTAGAACAAAAGTATC

FIGURE 4C

961 AAGTTGCACACAAGTAATCTGCCAGCTGACCTTGTGCGCACCTAACCAGTCACCACTT
1021 GCTATGGTATAGGATTATACTGATGTTCTTGAGGGATTCTGATGTGCTAGGCATGGITC
1081 TAAGTACTTTACTTGATTATCCCATTAAACTTAGAACAAACCCGTGAGATAAGTAGT
1141 TATTATCCTCATTTACACATGAGGGACCGAAGGATAGAAAAGTTATTTCAAAGGTCT
1201 TGCAAGTTAATAAAATGGCAGAGTGGCATTCAAGTCCAGGTAGTCATATTCCAGAGGCCAC
1261 GGTTTAACCACCTAGGCTTAGAGCTCCGCCGCGCCCTATGCATTATGTTACAAATGC
1321 CAATCTAGATGCTCCTCTTTGTATAAAGTCACTGACATTCTTAGAGTGGTTGGGTG
1381 CATCCAAAAATGTATAAAAATTATTATAATAAAACTTATTACTGCTTGTAGGGTAATT
1441 ACAGTTACTTACCCATTCTGCTTGGAACATGAGCCTGGAGACCCATGGCAGTCATAT
1501 GCCTCCCTATGCAGTGAAGGCCCTAGCAGTGTAAACAAATTGCTGAGATCCCACGGAGT
1561 CTTTCAAAAATCTCTGTAGAGTTAGTCTCTCTCTCTGAGAAGTTCTCCTGC
1621 CTGCATAACCATTCACTAGGGAGTACTTACAAGCATGAAGGATATTAGGGTAAGTGGCT
1681 AATTATAAAATCTACTCTAGAGACATATAATCATACAGATTATTCTATAAAATTTCAGTG
1741 CTGTCCTCCACATTAAATTGCAATTGCTCAAACGTAGAATGCCCTACATTCCCCCA
1801 CCCCAATTGCTATTCCCTATTAAAATAGAAAATTAGGCAAGATAACATTATATGCG
1861 TTCCCTCTCCTGAAATTATAACATTCTAAACTTACCCACGTAGGGACTACTGAATCCAA
1921 CTGCCAACATAAAAAGACTTTATTAGTAGAGGCTACCTTCCCCCAGTGACTCTT
1981 TTCTACAACGTGCTTGTCAAGTTGGTAATTCACTTATGATTCTTAATGTTCTCTGGTG
2041 AATTATTATTATCTGGACCTCTTTTTTTTTAAAGACAGAGTCTGCTCTGTCA
2101 CCCATTGCTCTCGTTGGCAACAAGAGTGAAACTCTGCTCTGCAAAAAAAAAAAATG
2161 AGGTTAAGACAGTTTGTCAATTACTGGTGGGATCTGGTCACACAAGATAGCATTAAACG
2221 TGACATGGCACATAAAATTGGTTAAAAAATTGGTTAAATTGCGTAATGTAAGGCC
2281 CAACAAACACTTATGCAAGATTGGAAATGTATCTCAAATTCAAGATTAAATAACATGTA
2341 AAGATCCTCTGTAaaaaaaaaaaaaaaaaaaaaaaa

FIGURE 4C

1 ACGCGGGGGATCCAGCTTGGTAGGCAGGGAAAGCAGCTGGAGTGCACCGCTACGGCAGC
 61 CACCCCTGCAACGCCAGTCGGAGAGCTAAGGGCAAGTCCTGAGGTGGGCCAGGAGAAA
 121 GAAGGCAGGAGACATTGTCAGGATATTCTGGTGATCTTGAAGTGTCCGTATCATG
 181 GAATCAATCTCTATGATGGGAAGGCCCTAAGAGCCTAGTGAACATTGTTACCTAATGGC
 241 ATAAATGGTATCAAAGATGCAAGGAAGGTCACTGTAGGTGTATTGGAAGTGGAGATTTT
 301 GCCAAATCCTGACCATTGACTTATTAGATGCGGCTATCATGTGGTCATAGGAAGTAGA
 361 AATCCTAAGTTGCTTCTGAATTTCCTCATGTGGTAGATGTCACTCATCATGAAGAT
 421 GCTCTCACAAAAACAAATAATATTTGGTGTATACACAGAGAACATTATACCTCCCTG
 481 TGGGACCTGAGACATCTGCTGTGGTAAAATCTGATTGAGCAATAACATGAGG
 541 ATAAACCAGTACCCAGAACATCCAATGCTGAATATTGGCTTCATTATTCCCAGATTCTTG
 601 ATTGTCAAAGGATTTAATGTTGCTCAGCTGGGCACITCAGTTAGGACCTAAGGATGCC
 661 AGCCGGCAGGTTATATATGAGCAACAATATTCAAGCGCGACAACAGGTTATTGAACCT
 721 GCCCGCCAGTTGAATTTCATTCCCATGACTTGGGATCCTTATCATCAGCCAGAGAGATT
 781 GAAAATTACCCCTACGACTTTACTTTCTGGAGAGGGCCAGTGGGTAGCTATAAGC
 841 TTGGCCACATTTCCTTGTCAACATGGCTACAGGTTATTGAGATGTGATTGCTAGA
 901 AACCAACAGAGTGACTTTACAAAATTCTATAGAGATTGTGAATAAAACCTTACCTATA
 961 GTGCCATTACTTTGCTCTCCCTAGTATACTTGCAGGTCTCTGGCAGCTGCTTATCAA
 1021 CTTTATTACGGCACCAGTATAGGAGATTCCACCTGGTGGAAACCTGGTACAGTGT
 1081 AGAAAACAGCTGGATTACTAAGTTTCTTCGCTATGGTCCATGGCTACAGCCTC
 1141 TGCTTACCGATGAGAAGGTCAAGAGAGATTGTTCTCAACATGGCTTATCAGCAGGTT
 1201 CATGCAAATATTGAAAATCTTGAATGAGGAAGAAGTTGGAGAATTGAAATGTATATC
 1261 TCCTTGGCATAATGAGCCTGGCTTACTTTCCCTGGCAGTCACTTCTATCCCTCA
 1321 GTGAGCAATGCCCTAAACTGGAGAGAATTCAAGTTTATTCACTACACTTGGATATGTC
 1381 GCTCTGCTCATAAGTACTTTCCATGTTTAATTATGGATGGAAACGAGCTTGTGAGGAA
 1441 GAGTACTACAGATTTATACACCACCAAACCTTGTCTTGTCTTGTGCTTACCTCAATT
 1501 GTAATTCTGGGTAAGGATTATTATTCCCTTCCATGTATAAGCGAAAGCTAAAACGAATT
 1561 AAAAAGGCTGGAAAAGGCCAATTCTGGAAGAAGGTATTGGAGGAACAATTCCCTCAT
 1621 GTCTCCCCGGAGAGGGTCACAGTAATGTGATGATAAATGGTTCACAGCTGCCATATAA
 1681 AGTTCTACTCATGCCATTATTATGACTTCTACGTTACAAGTATGCTGTCAA
 1741 TTATCGTGGGTTGAAACTTGTAAATGAGATTCAACTGACTTAGTGTAGAGTTCTT
 1801 CAAGTTAATTTCACAAATGTCATGTTGCAATATGAATTCTTAGTCAACATATTAT
 1861 TGTAATTAGGTATGTTTGTGTTGACAACGTGTAACCTGTTACTTATAT
 1921 TTCATAATCAGACAAAAACTTACAGTTAATAATATAGATATAATGTTAAAACAAATT
 1981 GCAAACCAGCAGAATTAAAGCTTTAAAATAATTCAATGGATATAACATTCTGAA
 2041 GATTAAGATTAAATTCAACTAAAAAGTAGAAATGCATTATTATACATTCTTAA
 2101 GAAAGGACACGTTATGTTAGCATCTAGGTAAAGGCTGCATGATGCACTTCTATATTCTC
 2161 TCATAAAATAGGATTGAAGGATGAAATTAAATTGTATGAAGCAATGTGATTATGAA
 2221 GACACAAATTAAAAAGACAATTAAACCTGAAATTATTTAAATATTGAGACATG
 2281 AAATACATACTGATAATACATACCTCATGAAAGATTATTCTTATTGTGTTACAGAGC
 2341 AGTTTCATTTCATATTAATATACTGATCAGGAAGAGGAGTCAGTAACATTGGCTTCCA
 2401 AAACTGCTATCTCTAACACGGTACCAATTCTAGGAACACTGTATACTAGTCTTACTTAGAA
 2461 CAAAAGTATCAAGTTGCACACAAGTAATCTGCCAGCTGACCTTGTGCGACCTTAACCA
 2521 GTCACCACTTGCTATGGTATAGGATTACTGATGTTGAGGGATTCTGATGTGCTA
 2581 GGCATGGTCTAAGTACTTTACTGTATTATCCCATTTAATACTTAGAACACACCCCGTGA
 2641 GATAAGTAGTTATTATCCTCATTTCACATGAGGGACCGAAGGATAGAAAAGTTATT
 2701 TCAAAGGTCTTGAGTTAATAATGGCAGAGTGAGCAATTCAAGTCCAGGTAGTCATA
 2761 CAGAGGCCACGGTTAACCACTAGGCTCTAGAGCTCCGCCGCCCCCTATGCAATTATG
 2821 TTCACAATGCCAATCTAGATGCTTCTCTTTGTATAAAGTCACTGACATTCTTAGAGT
 2881 GGGTTGGGTGCATCCAAAATGTATAAAAATTATTTATAATAACATTACTGCTTGT
 2941 AGGGTAATTCAAGTTACTTACCCATTCTTGTCTGGAACATGAGCCTGGAGACCCATGG
 3001 CAGTCCATATGCCCTATGCACTGAAAGGGCCCTAGCAGTGTAAACAAATTGCTGAGAT
 3061 CCCACGGAGTCTTCAAAATCTCTGTAGAGTTAGTCTTCTCCCTTCTTCTGAGAA
 3121 GTTCTCTGCCTGCATAACCATTCAATTAGGGAGTACTTTACAAGCATGAAGGATAATTAG
 3181 GTAAGTGGCTAATTATAAACTACTCTAGAGACATATAATCATACAGATTATTCAAAAA
 3241 TTTTCAGTGTGCTTCCACATTAAATTGCAATTGCTCAAACGTGAGAATGCCCTAC
 3301 ATTCCCCCCCACCCCAATTGCTATTCTTATTAAAAATGTATAAAAATTATTATAAT
 3361 AAACTTATTACTGCTTGTAGGGTAATTCAAGTTACTTACCCATTCTGCTTGGAACAT

FIGURE 4D

3421 GAGCCTGGAGACCCATGGCAGTCCATATGCCCTCCCTATGCAGTGAAGGGCCCTAGCAGTG
3481 TTAACAAATTGCTGAGATCCACGGAGTCCTTCAAAAATCTCTGTAGAGTTAGTCCTCTC
3541 CTTTTCTCTCCTGAGAAGTTCTCCTGCCTGCATAACCATTCAITAGGGAGTACTTTACA
3601 AGCATGAAGGATATTAGGGTAAGTGGCTAATTATAAATCTACTCTAGAGACATATAATCA
3661 TACAGATTATTCTAAAAATTTCAGTGCCTGCCTCCACATTAAATTGCATTTGCTCA
3721 AACTGTAGAATGCCCTACATCCCCCCCACCCCAATTGCTATTCTTATTAAAATAGAA
3781 AATTATAGGCAAGATAACAATTATATGCCTGCCTCTGAAATTATAACATTCTAAAC
3841 TTACCCACGTAGGGACTACTGAATCCAACGCCAACATAAAAAGACTTTTATTAGTAG
3901 AGGCTACCTTCCCCCAGTGACTCTTTCTACAACACTGCCCTGTCAGTTGGTAATTCA
3961 CTTATGATTTCTAATGTTCTCTTGGTGAATTATTATTATCTTGACCCCTTTTTTTTT
4021 TTTTTAAAGACAGAGTCCTGCTCTGTCACCCATTGCTCTCGTTGGCAACAAGAGTGAA
4081 ACTCTGTCTAAAAAAAAAAATGAGGTTAAAGACAGTTTGTCAATTACTGGTGGG
4141 ATCTGGTCACACAAGATAGCATTAAACGTGACATGGCACATAAAATTGGTAAAAAATT
4201 TGTTTTTAATTGCGTAATGTAAAAGCCAACAAACACTTTATGCAAGATTGGAATGTAT
4261 CTTCAAATTTCAGATTTAATAAACATGTAAGATCCTCTGTAAAAAAAAAAAAAAA
4321 AAAAAAAA

FIGURE 4D

1 ACGCGGGGGATCCAGCTTGGTAGGCGGGGAAGCAGCTGGAGTGCACCGCTACGGCAGC
 61 CACCCCTGCAACGCCAGTCGGAGAGCTAAGGGCAAGTCCTGAGGTTGGGCCAGGAGAAA

 1 M
 121 GAAGGCAAGGAGACATTGTCCCAGGATATTCTTGGTGATCTTGGAAAGTGTCCGTATCATG

 2 E S I S M M G S P K S L S E T C L P N G
 181 GAATCAATCTCTATGATGGGAAGCCCTAAGAGCCTTAGTGAACATTGTTACCTAATGGC

 22 I N G I K D A R K V T V G V I G S G D F
 241 ATAAATGGTATCAAAGATGCAAGGAAGGTCACTGTAGGTGTGATTGGAAGTGGAGATTT

 42 A K S L T I R L I R C G Y H V V I G S R
 301 GCCAAATCCTTGACCATTGACTTATTAGATGCGGCTATCATGTGGTCATAGGAAGTAGA

 62 N P K F A S E F F P H V V D V T H H E D
 361 AATCTTAAGTTGCTTCTGAATTTTCCATGTGGTAGATGTCACTCATCATGAAGAT

 82 A L T K T N I I F V A I H R E H Y T S L
 421 GCTCTCACAAAAACAAATATAATATTGTTGCTATACACAGAGAACATTATAACCTCCCTG

 102 W D L R H L L V G K I L I D V S N N M R
 481 TGGGACCTGAGACATCTGCTTGTGGTAAAATCCTGATTGATGTGAGCAATAACATGAGG

 122 I N Q Y P E S N A E Y L A S L F P D S L
 541 ATAAACCAGTACCCAGAATCCAATGCTGAATATTGGCTTCATTATCCCAGATTCTTGT

 142 I V K G F N V V S A W A L Q L G P K D A
 601 ATTGTCAAAGGATTTAATGTTGCTCAGCTTGGCACTTCAGTTAGGACCTAAGGATGCC

 162 S R Q V Y I C S N N I Q A R Q Q V I E L
 661 AGCCGGCAGGTTATATATGCAAGCAACAATTCAAGCGCAGAACAGGTTATTGAACCTT

 182 A R Q L N F I P I D L G S L S S A R E I
 721 GCCCGCCAGTTGAATTTCATTCCCATTGACTTGGATCCTTATCATCAGCCAGAGAGATT

 202 E N L P L R L F T F W R G P V V V A I S
 781 GAAAATTTACCCCTACGACTCTTACTTCTGGAGAGGGCAGTGGTGGTAGCTATAAGC

 222 L A T F F F L Y S F V R D V I H P Y A R
 841 TTGGCCACATTTTTTCTTATTCCCTTGTCAAGAGATGTCATTGATCCATATGCTAGA

 242 N Q Q S D F Y K I P I E I V N K T L P I
 901 AACCAACAGAGTGACTTTACAAAATTCCATAGAGATTGTGAATAAAACCTTACCTATA

 262 V A I T L L S L V Y L A G L L A A A Y Q
 961 GTTGCCTTACTTGTCTCCCTAGTATACCTTGCAGGTCTCTGGCAGCTGCTTATCAA

 282 L Y Y G T K Y R R F P P W L E T W L Q C
 1021 CTTTATTACGGCACCAAGTATAGGAGATTCCACCTTGGTGGAAACCTGGTACAGTGT

 302 R K Q L G L L S F F F A M V H V A Y S L
 1081 AGAAAACAGCTTGGATTACTAAGTTTTCTCGCTATGGCCATGTTGCCTACAGCCTC

 322 C L P M R R S E R Y L F L N M A Y Q Q V
 1141 TGCTTACCGATGAGAAGGTCAAGAGAGATAATTGTTCTCAACATGGCTTATCAGCAGGTT

FIGURE 4E

342 H A N I E N S W N E E E V W R I E M Y I
1201 CATGCAAATATTGAAAACCTTGGATGAGGAAGAAGTTGGAGAATTGAAATGTATATC

362 S F G I M S L G L L S L L A V T S I P S
1261 TCCTTGCGATAATGAGCCTGGCTTACTTTCCCTGGCAGTCACTTCTATCCCTCA

382 V S N A L N W R E F S F I Q S T L G Y V
1321 GTGAGCAATGCCTTAAACCTGGAGAGAATTCAAGTTTATTCAAGTCTACACTGGATATGTC

402 A L L I S T F H V L I Y G W K R A F E E
1381 GCTCTGCTCATAGTACTTCCATGTTAATTATGGATGGAAACGAGCTTTGAGGAA

422 E Y Y R F Y T P P N F V L A L V L P S I
1441 GAGTACTACAGATTTATACACCACAAACTTGTCTTGTCTTGTCTGCCCTCAATT

442 V I L G K I I L F L P C I S R K L K R I
1501 GTAATTCTGGTAAGATTATTTATTCCCTCATGTATAAGCCGAAAGCTAAACGAATT

462 K K G W E K S Q F L E E G I G G T I P H
1561 AAAAAAGGCTGGAAAAGGCCATTCTGAAGAAGGTATTGGAGGAACAATTCCCTCAT

482 V S P E R V T V M *
1621 GTCTCCCCGGAGAGGGTCACAGTAATGTGATGATAATGGTGTTCACAGCTGCCATATAA

FIGURE 4E

EXON_1 75bp
 1 GATCCAGCTGGTAGGCAGGGAAAGCAGCTGGAGTGCGACCGCCGCGCAGCCACCCCTGC
 61 AACCGCCAGTCGGAG

EXON_2 79bp
 1 AGAGCTAAGGGCAAGTCCCTGAGGTTGGGCCAGGAGAAAAGAAGGCAAGGAGACATTGTCC
 61 CAGGTAGGATGTGTCCCAG

EXON_3 525bp
 1 GATAATTCTTGGTGTCTGGAAAGTGTCCGTATCATGGAATCAATCTCTATGATGGGAAGC
 61 CCTAACAGACCTTAGTGAAACTTTTTTACCTAATGGCATAAAATGGTATCAAAGATGCAAGG
 121 AAGGTCACTGTAGGTGTGATGGAAAGTGGAGATTGTGCAAATCCTGACCAATTGACTT
 181 ATTAGATGCGGCATATCATGGGTCAAGGAAGTAGAAATCTAAGTTGCTCTGAATTT
 241 TTTCCCTCATGTGGTAGATGTCACATCATGAAGATGCTCTCACAAAAACAAATATAATA
 301 TTTGTGCTATAACACAGAGAACATTATAACCTCCCTGGGACCTGAGACATCTGCTTG
 361 GGTAAAATCCTGATTGATGTGAGCAATAACATGAGGATAAAACAGTACCCAGAATCCAAT
 421 GCTGAATAATTGGCTTCATTATTCCCAGATTCTTGTAAAGGATTTAATGTTGTC
 481 TCAGCTTGGGACTTCAGTTAGGACCTAAGGATGCCAGCCGGCAG

EXON_4 528bp
 1 GTTTATATATGCAGCAACAATATTCAAGCGCGACAACAGGTTATTGAACCTGCCGCCAG
 61 TTGAATTTCAITCCCATTGACTTGGGATCCTTATCATCAGCCAGAGAGATTGAAAATTAA
 121 CCCCTACGACTCTTACTCTCTGGAGAGGGCCAGTGGTGGTAGCTATAAGCTTGGCCACA
 181 TTTTTTTCCCTTATTCCCTTGTCAAGAGATGTGATTCCATATGCTAGAAACCAACAG
 241 AGTGACTIONTACAAAATTCTATAGAGAGATTGTGAATAAAACCTTACCTATAGTTGCCATT
 301 ACTTTGCTCTCCCTAGTATACTCGCAGGTCTTCTGGCAGCTGCTTATCAACTTTATTAC
 361 GGCACCAAGTATAAGGAGATTCCACCTGGTTGAAACCTGGTTACAGTGTAGAAAACAG
 421 CTTGGATTACTAAGTTTTCTCGTATGGCCATGTTGCCTACAGCCTCTGCTTACCG
 481 ATGAGAAGGTCAAGAGAGATATTGTTCTCAACATGGCTTATCAGCAG

EXON_5 165bp
 1 GTTCATGCAAATATTGAAAACCTTGGAAATGAGGAAGAAGTTGGAGAATTGAAATGTAT
 61 ATCTCCTTGGCATAATGAGCCTTGGCTTACTTCCCTCCTGGCAGTCACCTCTATCCCT
 121 TCAGTGAGCAATGCTTAAACTGGAGAGAATTCAAGTTATTCAAG

EXON_6 148bp
 1 TCTACACTTGGATATGTCGCTCTGCTCATAAGTACTTCCATGTTTAATTATGGATGG
 61 AAACGAGCTTTGAGGAAGAGTACTACAGATTATACACCACCAACTTGTCTTG
 121 CTTGTTTGCCCTCAATTGTAATTCTGG

EXON_7+UTR 718bp
 1 ATCTTTGCAGCTTGCAGATAACCCAGACTGAGCTGGAACTGGAATTGCTTCTATTG
 61 ACTCTACTTCTTAAAAGCGGCTGCCATTACATTCTCAGCTGCTTGCAGTTAGGTG
 121 TACATGTGACTGAGTGTGGCCAGTGAAGTCTCTCAAAGGAAGGCAGCATGTGT
 181 CCTTTTCATCCCTCATCTGCTGCTGGGATTGGATATAACAGGAGCCCTGGCAGCT
 241 GTCTCCAGAGGATCAAAGCCACACCCAAAGAGTAAGGCAGATTAGAGACCAGAAAGACCT
 301 TGACTACTCCCTACTTCCACTGCTTTCTGCATTAAAGCCATTGTAATCTGGGTGT
 361 GTTACATGAAGTAAAATTAAATTCTTCTGCCCTCAGTTCTTATCCTGATACCATTAA
 421 ACACTGTCTGAATTAACTAGACTGCAATAATTCTTCTTTGAAGCTTTAAAGGATAA
 481 TGTGCAATTCACTTAAATTGATTTCATTGTCATTAGTATACTCATTCTGCC
 541 TTGATCTTCAATTAGATATTGTATCTGCTTGGAAATATATTATCTTCTTTAACTGTG
 601 TAATTGGTAATTAACTCTGTAATCTCCAAATATTGCTATCAAATTACACACCATT
 661 GTTTCTATCATTCTCATAGATCTGCCTTATAAACATTAAATAAAAGTACTATTAA

1 GATCCAGCTTGGGTAGGCGGGGAAGCAGCTGGAGTGCACCGCCGCCAGCCACCCCTGC
61 AACCGCCAGTCGGAGAGAGCTAAGGGCAAGTCCTGAGGTGGGCCAGGAGAAAGAAGGC
121 AAGGAGACATTGTCCTCAGGTAGGATGTGTCCTCAGGATATTCTGGTGATCTGGAAGTGT
181 CCGTATCATGGAATCAATCTCTATGATGGGAAGCCCTAACAGCCTIAGTGAACACTTTTT
241 ACCTAATGGCATAAAATGGTATCAAAGATGCAAGGAAGGTACTGTAGGTGTGATTGGAAG
301 TGGAGATTTGCCAAATCTGACCATTGACTTATTAGATGCGGCTATCATGTGGTCAT
361 AGGAAGTAGAAATCTAACAGTTGCTTCTGAATTTCCTCATGTGGTAGATGTCACTCA
421 TCATGAAGATGCTCTCACAAAACAAATATAATATTGTTGCTATACACAGAGAACATTA
481 TACCTCCCTGTGGGACCTGAGACATCTGCTTGTGGTAAATCTGATTGATGTGAGCAA
541 TAACATGAGGATAAACCACTGACCTCAGAACATCCAATGCTGAATATTGGCTTCATTC
601 AGATTCTTTGATTGTCAAAGGATTTAACAGTTGCTCAGCTGGGACTTCAGTTAGGACC
661 TAAGGATGCCAGCCGGCAGGTTATATATGCAAGAACATATTCAAGCGGACAACAGGT
721 TATTGAACTTGCCCGCCAGTGAATTTCATTCCCATTGACTTGGGATCCTTATCATCAGC
781 CAGAGAGATTGAAAATTACCCCTACGACTCTTACTCTGGAGAGGGCCAGTGGTGGT
841 AGCTATAAGCTGGCCACATTTCCTTATTCCCTTGTCAAGAGATGTGATTCACTCC
901 ATATGCTAGAAACCAACAGAGTGAATTACAAAATTCTATAGAGATTGTGAATAAAC
961 CTTACCTATAGTTGCCATTACTTGCTCTCCCTAGTATACCTCGCAGGTCTCTGGCAGC
1021 TGCTTATCAACTTATTACGGCACCAAGTATAGGAGATTCCACCTTGGTTGAAACCTG
1081 GTTACAGTGTAGAAAACAGCTGGATTACTAAGTTTCTCGCTATGGCCATGTTGC
1141 CTACAGCCTCTGCTTACCGATGAGAACGTCAGAGAGATATTGTTCTCAACATGGCTTA
1201 TCAGCAGGTTCATGCAAATATTGAAAACCTTGGATGAGGAAGAAGTTGGAGAATTGA
1261 AATGTATATCTCCTTGGCATATGAGCCTTGGCTACTTTCCCTCCTGGCAGTCACITC
1321 TATCCCTTCAGTGAGCAATGCTTAAACTGGAGAGAATTCAAGTTTATTCACTCTACACT
1381 TGGATATGTCGCTCTGCTCATAAAGTACTTTCCATGTTTAATTATGGATGGAAACGAGC
1441 TTTTGAGGAAGAGTACTACAGATTATACACCACAAACTTGTCTTGCTTTGTTT
1501 GCCCTCAATTGTAATTCTGGATCTTGCAGCTTGCAGATAACCCAGACTGAGCTGGAAC
1561 TGGAATTGTCCTCCTATTGACTCTACTTCTTAAAGCGGCTGCCATTACATTCCCTCA
1621 GCTGTCCTTGCAGTTAGGTGTACATGTGACTGAGTTGGCCAGTGGAGATGAAGTCTCCT
1681 CAAAGGAAGGCAAGCAGTGTGCTTTTCCATCCCTCATCTTGCTGCTGGGATTGTGGATA
1741 TAACAGGAGCCCTGGCAGCTGCTCCAGAGGATCAAAGCCACACCCAAAGAGTAAGGCAG
1801 ATTAGAGACCAGAAAGACCTGACTACTTCCCTACTTCCACTGCTTTTCTGCATTAA
1861 GCCATGTAAACTGGGTGTGTTACATGAAGTGAAAATTAAATCTTCTGCCCTTCAGTT
1921 CTTTATCCTGATACCAATTAAACACTGTCATGAAATTAAACTAGACTGCAATAATTCTTCTT
1981 TGAAAGCTTTAAAGGATAATGTGCAATTACACATTAAATTGATTTCATTGTCAATTAA
2041 GTTATACTCATTTCTGCCCTGATCTTCAATTAGATATTGTATCTGCTTGGAAATTAA
2101 TTATCTCTTTTAACTGTGTAATTGGTAATTACTAAAACCTGTAATCTCCAAAATATT
2161 GCTATCAAATTACACACCATGTTCTATCATTCTCATAGATCTGCCCTATAAACATTAA
2221 AATAAAAAGTACTATTAA

FIGURE 4G

1 GATCCAGCTTGGGTAGGCGGGGAAGCAGCTGGAGTGCACGCCCGCAGCCACCCCTGCA
 62 ACCGCCAGTCGGAGAGAGCTAAGGGCAAGTCCTGAGGTTGGGCCAGGAGAAAGAAGGCA
 122 AGGAGACATTGTCCCAGGTAGGATGTGTCCCAGGATATTCTTGGTATCTTGGAAAGTGT
 M E S I S M M G S P K S L S E T C L
 182 CGTATCATGGAATCAATCTATGATGGAAGGCCCTAACAGCCTAGTGAAACTTGGTTA
 P N G I N G I K D A R K V T V G V I G S
 242 CCTAATGGCATAAAATGGTATCAAAGATGCAAGGAAGGTCACTGTAGGTGTGATTGGAAAGT
 G D F A K S L T I R L I R C G Y H V V I
 302 GGAGATTTGCCAAATCCTGACCATTGACTTATTAGATGCGGCTATCATGTGGTCATA
 G S R N P K F A S E F F P . H V V V D V T H
 362 GGAAGTAGAAAATCCTAAGTTGCTCTGAATTTCCTCATGTGGTAGATGTCACTCAT
 H E D A L T K T N I I F V A I H R E H Y
 422 CATGAAGATGCTCTCACAAAAACAAATATAATATTGTTGCTATACACAGAGAACATTAT
 T S L W D L R H L L V G K I L I D V S N
 482 ACCTCCCTGTGGACCTGAGACATCTGCTGTGGTAAACCTGATTGATGTGAGCAAT
 N M R I N Q Y P E S N A E Y L A S L F P
 542 AACATGAGGATAAACCAAGTACCCAGAACATCCAATGCTGAATATTGGCTTCATTATTCCA
 D S L I V K G F N V V S A W A L Q L G P
 602 GATTCTTGATTGTCAAAGGATTAATGTTGCTCAGCTGGGACTTCAGTTAGGACCT
 K D A S R Q V Y I C S N N I Q A R Q Q V
 662 AAGGATGCCAGCCGGCAGGTTATATATGCAAGAACATATTCAAGCGCAGAACAGGTT
 I E L A R Q L N F I P I D L G S L S S A
 722 ATTGAACCTGCCGCCAGTTGAATTCCATTGACTTGGGATCCTTATCATCAGCC
 R E I E N L P L R L F T L W R G P V V V
 782 AGAGAGATTGAAAATTACCCCTACGACTCTTACTCTGGAGAGGGCCAGTGGTGGTA
 A I S L A T F F F L Y S F V R D V I H P
 842 GCTATAAGCTTGGCCACATTTCCTTACTCTGGTCAAGAGATGTGATTCACTTCA
 Y A R N Q Q S D F Y K I P I E I V N K T
 902 TATGCTAGAAACCAACAGAGTGACTTTACAAAATCCCTATAGAGATTGTGAATAAAAC
 L P I V A I T L L S L V Y L A G L L A A
 962 TTACCTATAGTTGCCATTACTTTGCTCTCCCTAGTATACCTCGCAGGTCTCTGGCAGCT
 A Y Q L Y Y G T K Y R R F P P W L E T W
 1022 GCTTATCAACTTTATTACGGCACCAAGTATAGGAGATTCCACCTTGGTGGAAACCTGG
 L Q C R K Q L G L L S F F F A M V H V A
 1082 TTACAGTGTAGAAAACAGCTTGGATTACTAAGTTTTCTCGCTATGGCCATGTTGCC
 Y S L C L P M R R S E R Y L F L N M A Y

FIGURE 4H

1142 TACAGCCTCTGCTTACCGATGAGAAGGTCAAGAGATATTGTTCTAACATGGCTTAT
401 Q Q V H A N I E N S W N E E E V W R I E
1202 CAGCAGGTTCATGCAAATATTGAAAACCTCTGGAATGAGGAAGAAGTTGGAGAATTGAA
421 M Y I S F G I M S L G L L S L L A V T S
1262 ATGTATATCTCCTTGGCATAATGAGCCTTGGCTACTTTCCCTCCTGGCAGTCACTTCT
441 I P S V S N A L N W R E F S F I Q S T L
1322 ATCCCTTCAGTGAGCAATGCTTAAACTGGAGAGAATTCACTTTATTCACTACACTT
461 G Y V A L L I S T F H V L I Y G W K R A
1382 GGATATGTCGCTCTGCTCATAAGTACTTTCCATGTTTAATTATGGATGGAAACGAGCT
481 F E E E Y Y R F Y T P P N F V L A L V L
1442 TTTGAGGAAGAGTACTACAGATTATACACCACAAACTTGTCTTGCTTGT
501 P S I V I L D L L Q L C R Y P D -
1502 CCCTCAATTGTAATTCTGGATCTTGCAGCTTGCAGATAACCCAGACTGAGCTGGAAC

FIGURE 4H

EXON_1 75bp
 1 GATCCAGCTGGTAGGCAGGGAAAGCAGCTGGAGTGCACCGCCGCGCAGCCACCCCTGC
 61 AACCGCCAGTCGGAG

EXON_2 79bp
 1 AGAGCTAAGGGCAAGTCCTGAGGTTGGGCCAGGAGAAAGAAGGCAAGGAGACATTGTCC
 61 CAGGTAGGATGTGTCCCAG

EXON_3 525bp
 1 GATATTCTGGTATCTTGAAGTGTCCGTATCATGGAATCAATCTCTATGATGGGAAGC
 61 CCTAAGAGCCTTAGTGAACCTTTTACTAATGGCATAAAATGTATCAAAGATGCAAGG
 121 AAGGTCACTGTAGGTGTGATTGGAAGTGGAGATTTGCCAACCTCTGACCATTGACTT
 181 ATTAGATGCGGCTATCATGTGGTCATAGGAAGTAGAAAATCCTAAGTTGCTTCTGAATT
 241 TTCCCTCATGTGGTAGATGTCACTCATCATGAAGATGCTCTCACAAAAACAAATATAATA
 301 TTTGTTGCTATACACAGAGAACATTATAACCTCCCTGGGACCTGAGACATCTGCTTGTG
 361 GGTAAAATCCTGATTGATGTGAGCAATAACATGAGGATAAACAGTACCCAGAATCCAAT
 421 GCTGAATATTGGCTTCATTATCCCAGATTCTTGATTGTCAAAGGATTAAATGTTGTC
 481 TCAGCTGGGCACTTCAGTTAGGACCTAAGGATGCCAGCCGGCAG

EXON_4 528bp
 1 GTTTATATATGCAGCAACAATATTCAAGCGCGACAACAGGTTATTGAACCTGCCGCCAG
 61 TTGAATTTCATTCCCATTGACTCTGGGATCCTTATCATCAGCCAGAGAGATTGAAAATTAA
 121 CCCCTACGACTCTTACTCTCTGGAGAGGGCAGTGGTGGTAGTATAAGCTTGGCCACA
 181 TTTTTTTCTTTATTCCTTGTCAAGAGATGTGATTCATCCATATGCTAGAAACCAACAG
 241 AGTGACTTTACAAAATTCCTATAGAGATTGTGAATAAAACCTTACCTATAGTTGCCATT
 301 ACTTTGCTCTCCCTAGTATAACCTCGCAGGTCTCTGGCAGCTGCTTATCAACTTTATTAC
 361 GGCACCAAGTATAGGAGATTCCACCTGGTTGGAACCTGGTTACAGTGTAGAAAACAG
 421 CTTGGATTACTAAGTTTTCTTCGCTATGGCATGGTGCCTACAGCCTCTGCTTACCG
 481 ATGAGAAGGTCAAGAGAGATTGGTTCTCAACATGGCTTATCAGCAG

EXON_5 165bp
 1 GTTCATGCAAATATTGAAAACCTTGGAAATGAGGAAGAAGTTGGAGAATTGAAATGTAT
 61 ATCTCCTTGGCATAATGAGCCTGGCTTACTTTCCCTCCTGGCAGTCACCTCTATCCCT
 121 TCAGTGAGCAATGCTTTAAACTGGAGAGAATTCAAGTTTATTCAAG

EXON_7 and 3'UTR 718bp
 1 ATCTTTGCAGCTTGCAAGATACCCAGACTGAGCTGGAACCTGGAAATTGCTTCTTATTG
 61 ACTCTACTCTTAAAGCGCTGCCATTACATTCCCTCAGCTGCTTGCAGTTAGGTG
 121 TACATGTGACTGAGTGTGGCAGTGAGATGAAGTCTCTCAAAGGAAGGCAGCATGTG
 181 CCTTTTCTATCCCTCATCTGCTGCTGGATTGGATATAACAGGAGCCCTGGCAGCT
 241 GTCTCCAGAGGATCAAAGCACACCCAAAGAGTAAGGCAGATTAGAGACCAAGAACCT
 301 TGACTACTCCCTACTCCACTGCTTTCTGCATTAAAGCATTGTAATCTGGGTGTT
 361 GTTACATGAAGTAAAATTAAATTCTTCTGCCCTCAGTTCTTATCCTGATAACCATTTA
 421 ACACTGTCTGAATTAACTAGACTGCAATAATTCTTCTTTGAAAGCTTTAAAGGATAA
 481 TGTGCAATTCAACATTAAATTGATTTCATTGTCAATTAGTTATACTCATTCTGCC
 541 TTGATCTTCATTAGATATTGTATCTGCTGGAAATATATTATCTTCCTTTAACTGTG
 601 TAATTGGTAATTACTAAAACCTCTGTAATCTCCAAATATTGCTATCAAATTACACCCAT
 661 GTTTCTATCATGATCTGCCTTATAAACATTAAATAAAAAGTACTATTAA

FIGURE 4I

1 GGATCCAGCTTGGTAGGCGGGAAAGCAGCTGGAGTGCACCGCTACGGCAGCCACCC
61 CAACGCCAGTCGGAGAGCTAAGGGCAAGTCCGTAGGGTGGGCCAGGAGAAAGAAGCA
121 AGGAGACATTGTCAGGATATTCTGGTGATCTGGAAAGTGTCCGTATCATGGAATCAA
181 TCTCTATGATGGGAAGCCCTAACAGCCTAGTGAACATTGTTACCTAACGGATAATG
241 GTATCAAAGATGCAAGGAAGGTCAGTGTAGGTGTGATTGGAGATTGGCAAAAT
301 CCTTGACCATTGACTTATTAGATGCGGCTATCATGTGGCATAGGAAGTAGAAATCCTA
361 AGTTGCTCTGAATTTCCTCATGTGGTAGATGTCAGTCATGAAGATGCTCTCA
421 CAAAACAAATATAATATTGTTGCTATACACAGAGAACATTACCTCCGTGGGACC
481 TGAGACATCTGCTTGTGGTAAACCTGATTGATGTGAGCAATAACATGAGGATAAAC
541 AGTACCCAGAACATGCTGAATATTGGCTTCATTAACTCCAGATTCTTGATTGTC
601 AAGGATTAATGTTGTCAGCTGGGACTTCAGTTAGGACCTAACGGATGCCAGCCGGC
661 AGGTTATATGCAAGAACATATTCAAGCGCAGAACAGGTATTGAACTTGCCCCGCC
721 AGTTGAATTTCATCCCATTGACTTGGATCCTTATCATCAGCAGAGAGATTGAAAATT
781 TACCCCTACGACTCTTACTTCTGGAGAGGGCCAGTGGTAGCTATAAGCTTGGCCA
841 CATTTTTTCCCTTATTCCCTTGTCAAGAGATGTGATTCCATATGCTAGAAACCAAC
901 AGAGTGACTTTACAAAATTCCCTATAGAGATTGTGAATAAAACCTTACCTATAGTTGCCA
961 TTACTTGTCTCCCTAGTATACCTTGAGGTCTCTGGCAGCTGCTTATCAACTTTATT
1021 ACGGCACCAAGTATAGGAGATTCCACCTTGGTGGAAACCTGGTTACAGTAGAAAAC
1081 AGCTTGGATTACTAAGTTTTCTCGCTATGGTCCATGGCTACAGCCTCTGCTTAC
1141 CGATGAGAAGGTCAAGAGAGATTGTTCTCAACATGGCTTATCAGCAGGTTCATGCAA
1201 ATATTGAAAACCTTGGATGGAGGAAGTGGAGAATTGAAATGTATATCTCCATTG
1261 GCATAATGAGCCTTGGCTTACTTTCCCTCCGGCAGTCACCTCTATCCCTCGGTGAGCA
1321 ATGCTTAAACTGGAGAGAACCTCAGTTTATTCAAGATCTTGTCAAGCTTGCAGATAACCC
1381 AGACTGAGCTGAAACTGGAATTGCTTCCATTGACTCTACTTCTTTAAAGCGGCTGC
1441 CCATTACATTCCCTCAGCTGTCTTGAGCTAGGTGTACATGTGACTGAGTGTGGCCAGT
1501 GAGATGAAGTCCCTCAAAGGAAGGCAAGCATGTGCTCTTTCATCCCTCATCTTGCTG
1561 CTGGGATTGTGGATATAACAGGAGCCCTGGCAGCTGCTCCAGAGGATCAAAGCCACACCC
1621 AAAGAGTAAGGCAAGATTAGAGACCAGAAAGACCTGACTACTTCCCTACTTCCACTGCTT
1681 TTTCCCTGCAATTAAAGCCATTGTAATCTGGTGTGTTACATGAAGTGAAAATTAAATTCTT
1741 TCTGCCCTTCAGTTCTTATCTGATACCATTTAACACTGTGCTGAATTAAACTAGACTGCA
1801 ATAATTCTTCTTGTAAAGCTTTAAAGGATAATGTGCAATTACATTAAATTGATT
1861 TCCATTGTCAATTAGTTATACTCATTTCTGCTGCTTGTATCTTCAATTAGATAATTGTAT
1921 CTGCTTGGAAATATATTCTTCTTAACTGTGTAATTGGTAATTACTAAACCTCTGTA
1981 ATCTCCAAAATATTGCTATCAAATTACACACCATGTTCTATCATTCTCATAGATCTGC
2041 CTTATAAACATTAAATAAAAAGTACTATTACCAAAAAAAAAAAAAAA
2101 AA

FIGURE 4J

1GGATCCAGCTTGGTAGGCAGGGAAAGCAGCTGGAGTGCAGCCACCGCTACGGCAGCCACCCCTGCA
 63 ACCGCCAGTCGGAGAGCTAAGGGCAAGTCCTGAGGTTGGGCCAGGAGAAAGAAGGCAAG

 1 M E S I
 123 GAGACATTGTCCCAGGATATTCTTGGTATCTTGGAAAGTGTCCGTATCATGGAATCAATC

 5 S M M G S P K S L S E T C L P N G I N G
 183 TCTATGATGGGAAGCCCTAAGAGCCTAGTGAAACTTGTACCTAATGGCATAAATGGT

 25 I K D A R K V T V G V I G S G D F A K S
 243 ATCAAAGATGCAAGGAAGGTCACTGTAGGTGTGATTGGAAGTGGAGATTTGCCAAATCC

 45 L T I R L I R C G Y H V V I G S R N P K
 303 TTGACCATTGACTTATTAGATGCGGCTATCATGTGGTCATAGGAAGTAGAAATCCTAAG

 65 F A S E F F P H V V D V T H H E D A L T
 363 TTTGCTTCTGAATTTCCTCATGTGGTAGATGTCACTCATGAAGATGCTCTCAC

 85 K T N I I F V A I H R E H Y T S L W D L
 423 AAAACAAATATAATATTGTTGCTATACACAGAGAACATTACCTCCCTGTGGACCTG

 105 R H L L V G K I L I D V S N N M R I N Q
 483 AGACATCTGCTTGGTAAATCCTGATTGATGTGAGCAATAACATGAGGATAAACAG

 125 Y P E S N A E Y L A S L F P D S L I V K
 543 TACCCAGAATCCAATGCTGAATATTGGCTTCATTATTCCAGATTCTTGATTGTCAA

 145 G F N V V S A W A L Q L G P K D A S R Q
 603 GGATTAAATGTTGTCAGCTTGGCACTTCAGTTAGGACCTAAGGATGCCAGCCGGCAG

 165 V Y I C S N N I Q A R Q Q V I E L A R Q
 663 GTTTATATATGCAGCAACAATATTCAAGCGCAGAACAGGTTATTGAACCTGCCGCCAG

 185 L N F I P I D L G S L S S A R E I E N L
 723 TTGAATTTCATTCCATTGACTTGGGATCCTTATCATCAGCCAGAGAGATTGAAAATTAA

 205 P L R L F T F W R G P V V V A I S L A T
 783 CCCCTACGACTCTTACTTTCTGGAGAGGGCCAGTGGTAGCTATAAGCTTGGCCACA

 225 F F F L Y S F V R D V I H P Y A R N Q Q
 843 TTTTTTTCTTATTCTCTTGTCAGAGATGTGATTCCATATGCTAGAAACCAACAG

 245 S D F Y K I P I E I V N K T L P I V A I
 903 AGTGAACCTTACAAATCCTATAGAGATTGTGAATAAAACCTACCTATAGTTGCCATT

 265 T L L S L V Y L A G L L A A A Y Q L Y Y
 963 ACTTTGCTCTCCCTAGTATAACCTTGCAGGTCTTCTGGCAGCTGCTTATCAACTTATTAC

 285 G T K Y R R F P P W L E T W L Q C R K Q
 1023 GGCACCAAGTATAGGAGATTCCACCTGGTTGGAAACCTGGTACAGTGTAGAAAACAG

 305 L G L L S F F F A M V H V A Y S L C L P
 1083 CTTGGATTACTAAGTTTTCTCGCTATGGTCATGTTGCCTACAGCCTCTGCTTACCG

 325 M R R S E R Y L F L N M A Y Q Q V H A N

FIGURE 4K

1143 ATGAGAAGGTCAGAGAGATTTGTTCTCAACATGGCTTATCAGCAGGTTCATGCAAAT
345 I E N S W N E E E V W R I E M Y I S F G
1203 ATTGAAAACCTTGGAAATGAGGAAGAAGTTGGAGAATTGAAATGTATATCTCCTTGCG
365 I M S L G L L S L L A V T S I P S V S N
1263 ATAATGAGCCTTGGCTTACTTCCCTCCTGGCAGTCACTTCTATCCCTCGGTGAGCAAT
385 A L N W R E F S F I Q I F C S F A D T Q
1323 GCTTAAACTGGAGAGAACATTAGATCTTGCAGCTTGAGATAACCCAG
405 T E L E L E F V F L L T L L L *
1383 ACTGAGCTGGAACCTGGAAATTGTCTTCTTATTGACTCTACTTCTTAAAAGCGGCTGCC
1443 ATTACATTCTCAGCTGCTTGCAGTTAGGTGTACATGTGACTGAGTGTGGCCAGTGA
1503 GATGAAGTCTCCTCAAAGGAAGGCAGCATGTGTCTTTTCACTCCCTCATCTGCTGCT
1563 GGGATGTGGATATAACAGGAGCCCTGGCAGCTGCTCCAGAGGATCAAAGCCACACCAA
1623 AGAGTAAGGCAGATTAGAGACCAGAAAGACCTTGACTACTTCCCTACTTCCACTGCTTT
1683 TCCTGCATTTAACGCCATTGTAATCTGGGTGTGTTACATGAAGTGAATTAATTCTTC
1743 TGCCCTTCAGTTCTTATCCTGATACCATTAAACACTGTCTGAATTAAACTAGACTGCAAT
1803 AATTCTTCTTTGAAAGCTTAAAGGATAATGTGCAATTACATTTAAATTGATTTCT
1863 CATTGTCAATTAGTTACTCATTTCTGCCTTGATCTTCATTAGATATTGTATCT
1923 GCTTGGAAATATATTATCTCTTTAACCTGTGTAATTGGTAATTACTAAAACCTGTAAAT
1983 CTCCAAAATATTGCTATCAAATTACACACCATGTTCTATCATTCTCATAGATCTGCCT
2043 TATAAACATTAAATAAAAAGTACTATTACCAAAAAAAAAAAAAAA

FIGURE 4K

1 M E K T C I D A L P L T M N S S E K
 1 ACAGATCTATGGAGAAAACTTGTATAGATGCACCTCCTACTATGAATTCTCAGAAAAG
 19 Q E T V C I F G T G D F G R S L G L K M
 63 CAAGAGACTGTATGTATTTGGAACTGGTATTTGGAAAGATCACTGGGATTGAAAATG
 39 L Q C G Y S V V F G S R N P Q K T T L L
 123 CTCCAGTGTGGTTATTCTGTTGGAAAGTCGAAACCCCCAGAAGACCACCCACTG
 59 P S G A E V L S Y S E A A K K S D I I I
 183 CCCAGTGGTGCAGAAGTCTTGAGCTATTAGAAGCAGCCAAGAAGTCTGACATCATATAATC
 79 I A I H R E H Y D F L T E L T E V L N G
 243 ATAGCAATCCCACAGAGAGCATTATGATTTCTCACAGAATTAACGAGGTTCTCAATGGA
 99 K I L V D I S N N L K I N Q Y P E S N A
 303 AAAATATTGGTAGACATCAGCAACAACCTCAAATCAATATCCAGAATCTAATGCA
 119 E Y L A / T H L V P G A H V V V K A F N T I S
 363 GAGTACCTTGTCTATTGGTGCAGGAGCCACGTGGTAAAGCATTAAACACCATCTCA
 139 A W A L Q S G A L D A S R Q V F V C G N
 423 GCCTGGCTCTCCAGTCAGGAGCACTGGATGCAAGTCGGCAGGTGTTGTGTGGAAAT
 159 D S K A K Q R V M D I V R N L G L T P M
 483 GACAGCAAAGCCAAGCAAAGAGTGATGGATATTGTTGTAATCTGGACTTACTCCAATG
 179 D Q G S L M A A K E I E K Y P L Q L F P
 543 GATCAAGGATCACTCATGGCAGCAAAGAAATTGAAAAGTACCCCTGCAGCTATTCCA
 199 M W R F P F Y L S A V L C V F L F F Y C
 603 ATGTGGAGGTTCCCTCTATTGTCTGCTGTGTCTCTGTTCTATTGT
 219 V I R D V I Y P Y V Y E K K D N T F R M
 663 GTTATAAGAGACGTAATCTACCCATTGTTATGAAAGAAAGATAATACATTCTGTATG
 239 A I S I P N R I F P I T A L T L L A L V
 723 GCTATTCCATTCAAATCGTATCTTCCAATAACAGCACTTACACTGCTTGCTTGGTT
 259 Y L P G V I A A I L Q L Y R G T K Y R R
 783 TACCTCCCTGGTATTGCTGCCATTCTACAACTGTACCGAGGCACAAATACCGTCGA
 279 F P D W L D H W M L C R K Q L G L V A L
 843 TTCCCAGACTGGCTTGACCACTGGATGCTTGCAGCAGCTGGCTGGTAGCTCTG
 299 G F A F L H V L Y T L V I P I R Y Y V R
 903 GGATTTGCCTCCTCATGTCTACACACTTGTGATTCTTATTCGATATTATGTACGA
 319 W R L G N L T V T Q A I P / L K K E N P F S
 963 TGGAGATTGGAAACTAACCGTTACCCAGGCAATACCAAGAAGGAGAATCCATTAGC
 339 T S S A W L S D S Y V A L G I L G F F L
 1023 ACCTCCTCAGCCTGGCTCAGTGATTGATATGTGGCTTGGAAATACTGGGTTTTCTG
 359 F V L L G I T S L P S V S N A V N W R E

FIGURE 4L

1083 TTTGTACTCTGGGAATCACCTCTTGCACATGTTAGCAATGCAGTCAACTGGAGAGAG
379 F R F V Q S K L G Y L T L I L C T A H T
1143 TTCCGATTGTCCAGTCAAACCTGGGTATTGACCCTGATCTGTGTACAGCCCACACC
399 L V Y G G K R F L S P S N L R W Y L P A
1203 CTGGTGTA CGGTGGGAAGAGATTCCCTCAGCCCTTCAAATCTCAGATGGTATCTCCTGCA
429 A Y V L G L I I P C T V L V I K F V L I
1263 GCCTACGTGTTAGGGCTTATCATTCCCTGCACTGTGCTGGT GATCAAGTTGTCCTAATC
439 M P C V D N T L T R I R Q G W E R N S K
1323 ATGCCATGTGTAGACAACACCC TTACAAGGATCCGCCAGGGCTGGAAAGGA ACTCAAAA
459 H -
1383 CACTAGCTCGAGGT

FIGURE 4L

1ACCCCTCGCCGGGACCTTCAGCTGCCGGTCGCTCCAGCAGGGCCGCAGAGGTT
 63 AAGCGATTCTCCTGCTTCAGCCTCCGGAGTAGCTGGATTACAGGCACGTGCCAACACAC
 1 M P E E M D K P L I S L H L V D
 123 CCAGCCACCAAAATGCCAGAAGAGATGGACAAGCCACTGATCAGCCTCCACCTGGTAGC
 17 S D S S L A K V P D E A P K V G I L G S
 183 AGCGATAGTAGCCTGCCAAGGTCCCCATGAGGCCCCAAAGTGGCATCCTGGTAGC
 37 G D F A R S L A T R L V G S G F K V V V
 243 GGGGACTTTGCCCGCTCCCTGCCACAGCCTGGTGGCTCTGGCTCAAAGTGGTAGC
 57 G S R N P K R T A R L Y P S A A Q V T F
 303 GGGAGCCGCAACCCCAAACGCACAGCCAGGCTGTATCCCTCAGCGGCCAAGTGACTTC
 77 Q B E A V S S P E V I F V A V F R E H Y
 363 CAAGAGGAGGCAGTGAGCTCCCGGAGGTCAATCTTGCTGTGTTCCGGGAGCACTAC
 97 S S L C S L S D Q L A G K I L V D V S N
 423 TCTTCACTGTGCAAGTCTCACTGACCAGCTGGCGGGCAAGATCCTGGATGTGAGCAC
 117 P T E Q E H L Q H R E S N A E Y L A S L
 483 CCTACAGAGCAAGAGCACCTTCAGCATCGTGAGTCCAATGCTGAGTACCTGGCTCCCTC
 137 F P T C T V V K A F N V I S A W T L Q A
 543 TTCCCCACTTGACAGTGGTCAAGGCCTCAATGTCATCTGCTGGACCCCTGCAGGCT
 157 G P R D G N R Q V P I C G D Q P E A K R
 603 GGCCCAAGGGATGGTAACAGGCAGGTGCCATCTGGTGGACAGCCAGAAGCAGCT
 177 A V S E M A L A M G F M P V D M G S L A
 663 GCTGTCTCGGAGATGGCGCTGCCATGGCTCATGCCGTGGACATGGATCCCTGGCG
 197 S A W E V E A M P L R L L P A W K V P T
 723 TCAGCCTGGGAGGTGGAGGCCATGCCCTGCGCCTCTCCGGCTGGAAAGGTGGCCACC
 217 L L A L G L F V C F Y A Y N F V R D V L
 783 CTGCTGGCCCTGGGCTCTCGCTGCTATGCCACACTTCGTCCGGACGTTCTG
 237 Q P Y V Q E S Q N K F F K L P V S V V N
 843 CAGCCCTATGTGAGGAAGCCAGAACAGTCTCAAGCTGCCGTGTGGCAAC
 257 T T L P C V A Y V L L S L V Y L P G V L
 903 ACCACACTGCCGTGCGTGGCCTACGTGCTGACTCGTGTACTTGCCCGGGCTGCTG
 277 A A A L Q L R R G T K Y Q R F P D W L D
 963 GCGGCTGCCCTGCAAGCTGCGCGGGACCAAGTACCGCCTCCCGACTGGCTGGAC
 297 H W L Q H R K Q I G L L S F F C A A L H
 023 CACTGGCTACAGCACCGCAAGCAGATGGGCTGCTCAGCTTCTGCCCGCCCTGCAC
 317 A L Y S F C L P L R R A H R Y D L V N L
 .083 GCCCTCTACAGCTCTGCTGCCGTGCCCGGCCACCGCTACGACCTGGTCAACCTG
 337 A V K Q V L A N K S H L W V E E E V W R
 .143 GCAGTCAAGCAGGTCTGGCCAACAAGAGGCCACCTCTGGGTGGAGGAGGTCTGGCGG
 357 M E I Y L S L G V L A L G T L S L L A V
 .203 ATGGAGATCTACCTCTCCCTGGAGTGCTGGCCCTCGGCACGTTGTCCCTGCTGGCCGTG

FIGURE 4M

377 T S L P S I A N S L N W R E F S F V Q S ·
 1263 ACCTCACTGCCGTCCATTGCAAACCTCGCTCAACTGGAGGGAGTTCACTGGCTTCAGCTTCAGTCC

 397 S L G F V A L V L S T L H T L T Y G W T
 1323 TCACTGGGCTTGTGGCCCTCGTGCTGAGCACACTGCACACGCTCACCTACGGCTGGACC

 417 R A F E E S R Y K F Y L P P T F T L T L
 1383 CGCGCCTTCGAGGAGAGCCGCTACAAGTTCTACCTGCCTCCCACCTTCAGCTCACGCTG

 437 L V P C V V I L A K A L F L L P C I S R
 1443 CTGGTGCCCTCGCTCGTCATCCTGGCAAAGCCCTGTTCTCCCTGCCCTGCATCAGCCGC

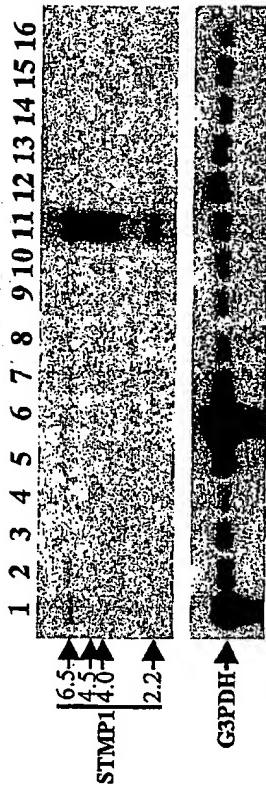
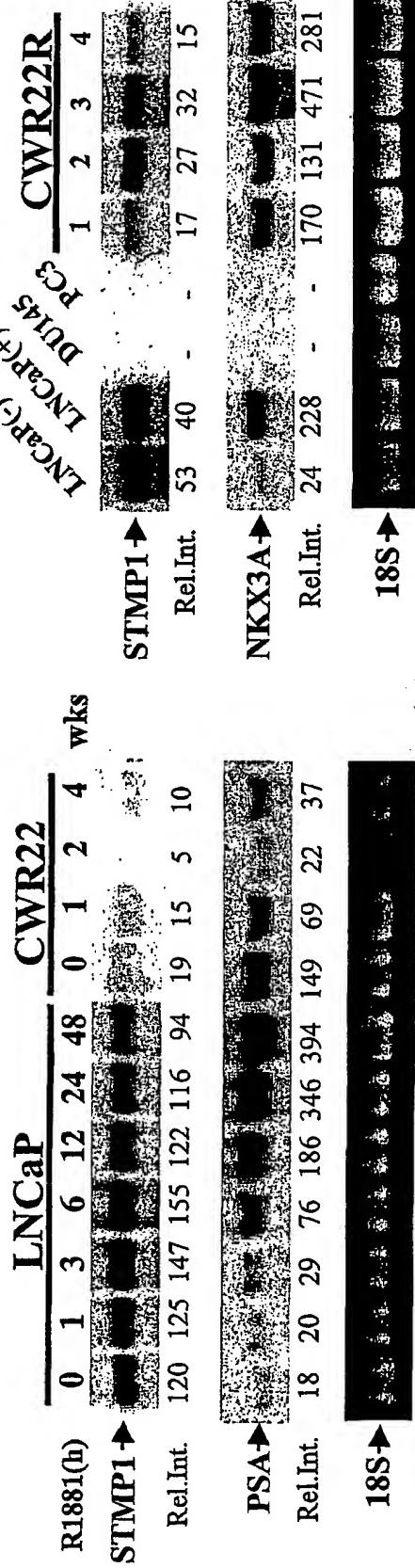
 457 R L A R I R R G W E R E S T I K F T L P
 1503 AGACTGCCAGGATCCGGAGAGGGCTGGGAGAGGGAGAGCACCATCAAGTTCACGCTGCC

 477 T D H A L A E K T S H V -
 1563 ACAGACCACGCCCTGGCCGAGAAGACGAGCCACGTATGAGGTGCCCTGCCCTGGGCTGG

 1623 ACCCCGGGCACACGAGGGAGCGGTGCCCTGAGCCGTTAGGTTTCCTTCTTGGTGGTGC
 1683 AAAGTGGTATAACTGTGTGCAAATAGGAGGTTGAGGTCAAATTCCCTGGGACTCAAATG
 1743 TATGCAGTAATTCAGAAATGATATAACACACATATGTGTATATGTATTTACATATAATTC
 1803 ACATATATAACAGGATTGCAATTACATAGCTAGCTAAAAAGTTGGGTCTGAGATT
 1863 TCAACTTGTAGATTTAAAACAAGTGGCTACGTTAACAGAGAGCAGATCATGCTATTG
 1923 TGACATTTGAGAGATATAACACACATTTGTACAGAACAGGGCTGTGCTGGTGGGGT
 1983 TCGATTTATCCCTGCCACCCCCATCCCCACAACCTTCCCTTGCACCTCCCCAAGGCTC
 2043 TTGCGAGAGCTAGGGCTCTGAAGGGGAGGCAACGGCTCTGCCAGAGCCATCCCTG
 2103 GAGCATGTGAGCAGCGGTGGTCTTCCCTCACCTGGGAGCTGTGCTGCCCTTGGGG
 2163 GGGGAGGAAAATCAGGCAGTCGGCTGGAGTCTGTGCTGCCCTTGGGGGGGG
 2223 AGGATGGAGGGATTGGGCTGAAGCTGCCACCTCATCTGCTGAGTGGGGGAGACATT
 2283 TTCCCTGAAAGTCAGAACCATAGAGCCTGCAAATGGATCCTCTGTGAGAGTGACG
 2343 TCACCTCCTTCCAGAGCCATTAGTGGCTGGCTGGAAACAAGTGTAAATTCCCTCCC
 2403 TCCTTAACTGGCAGTCGGCTGGAGTGGCTTAAACCAACTGTGCCCTTCACCCCTTCC
 2463 CAGTTGAACGACTCCAGGAAGGCCAGAACCTTGGAAATCAGCCCCAAGGGGG
 2523 AGAGCAAGAGAAAACACTCTAGGGAGTAAAGCTCCCCGGCGTCAGAGTTGAGCCCTG
 2583 TGGCTGAAAGACTGTCTTCAGGAAGCTCAGTGGCTGGAGAAAATATTGGGACTCCA
 2643 GTCTCTGGCAGAGGCCAGAACACTGGCTCCAACCTCCTCATGGGCATT
 2703 ACACCTCAAACAGTGGGAGCAACTTCCACAAAGCTACAAACCTAAAATGCTGCTG
 2763 CCCCAAAGCACAAGAGGGAGAGCACCGCCGGGGCACAGGACGCTGTGCTCCAGTCAC
 2823 AGGCCATCCTGCTGCTCCACTGACTCTAGCTTACTTCCCTGTGAAGAAAACAGGTGT
 2883 TCTCGGCTGAGCCCCAACCTCTGCAGAACAGGTGATCTGCCACAGAAAAGCATT
 2943 TTGAAGACAAAGAGGGTAGGGTCTTCATGAGTCCTCTGGGCAAAGGCATCTCTGATG
 3003 GAAGGAAGAGAGTAGGGCCAGTGAAGGCTGCCAGAGAGAAATGTCACAGATGAGGCTGCC
 3063 CCTGCCCCCTCCCCGCCAGGGAGGTTCTAGGCTCATGAGCTCATGTCATGAGCACATAAGGGTT
 3123 CTCAGTAAAAGCAGGAGAGAACGCCCAGTGAAGGAGTAGCTCATAGGCACATGACCGA
 3183 TCGAGGGAGGCCATGCCGGGAAGCTCTTCTGCAGGTATTTCCATCTGCTGCC
 3243 GGCTGAGGGCAGAAAATTGTCTCATAAATTGGCACTGATGGAGCATCAGCTGTGGG
 3303 CAGAGAGCCTGCTGAGAAGGGGGCAGGTAAGAGAGATTAGCATTGCCCTGGCATA
 3363 ACAAGGGCCCACGATCCCTACTATGAGGGAGAGGAGCATGGCAATGGAGACCC
 3423 ACCAATGATCCCAACCCGGTGGGTACTGGCTGCCCTGGGCCAGGGAAATGGCTCC
 3483 TTATACCAAAGATGCTGGCACATAGCAGAACCCAGTGCAGCTCCCTTCCCACCCAC
 3543 CTCGGCTGAAGGTGCTCAAGAGGGAGCAATTATAAGGTGGTGGCAGGAGGGAAACAGG
 3603 TGCCACCTGCTGGACAATCACAGAACGGCAGGGCTGTGACTGGCCCTGACTGTG
 3663 CGTCCACTGCTGCTTCCCTACCTCACCGCTACTGGCAGCAGCATCCGAGAGCACAT
 3723 CATCTCCACAGCCTGGTAAATTCCATGTCCTGGGTACAAAAGTGCCTCAACGACATG
 3783 CTCGGAAATCCCAAATGCCACAGTGTGAGGTGATATCTAAAATCTATGCC
 3843 AGTCTGTGTTTTTTAACCTGGTAGACGGTATAAAAGCAGTGCAAATAAACACCT
 3903 AACCTTCIGC

FIGURE 4M

Figure 5

A**B****Figure 6**

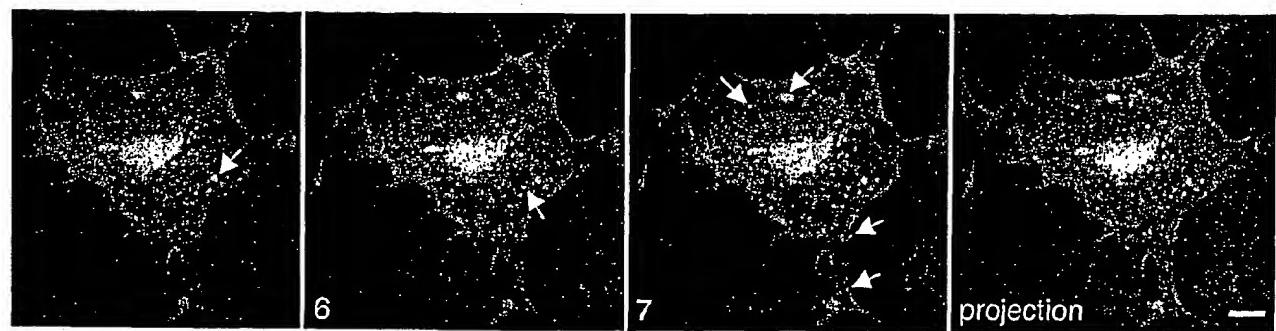


Figure 7A

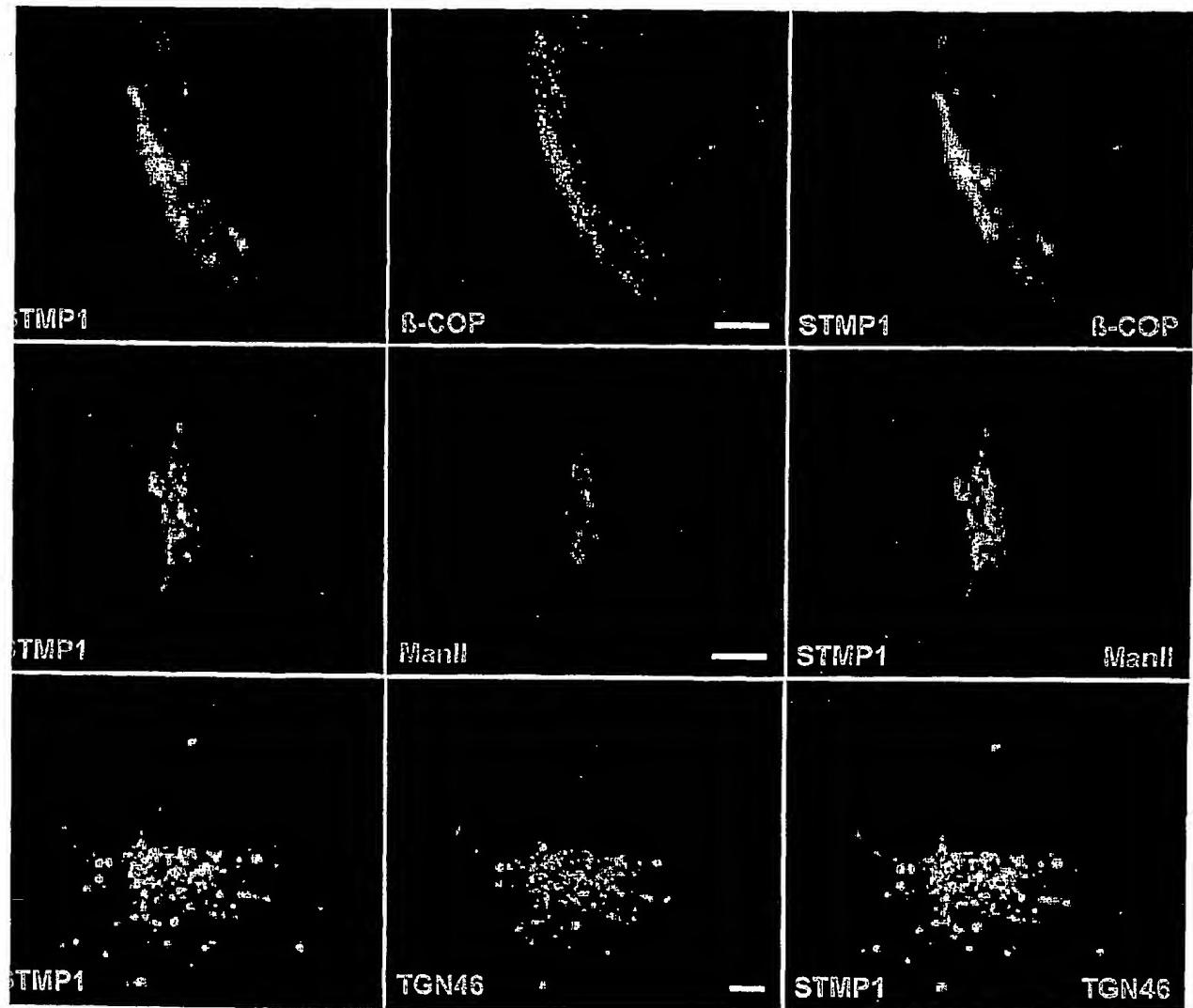


Figure 7B

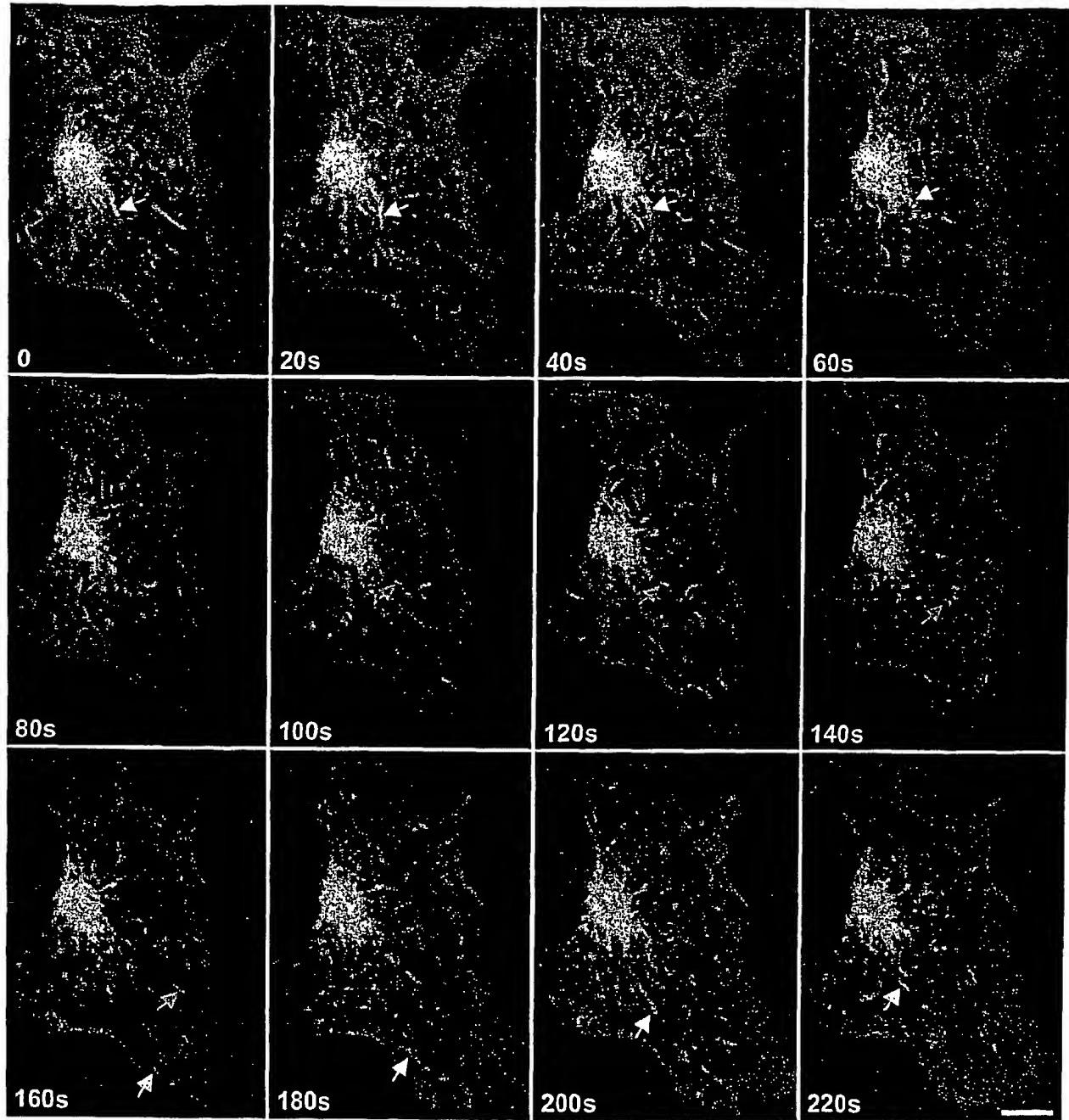


Figure 8

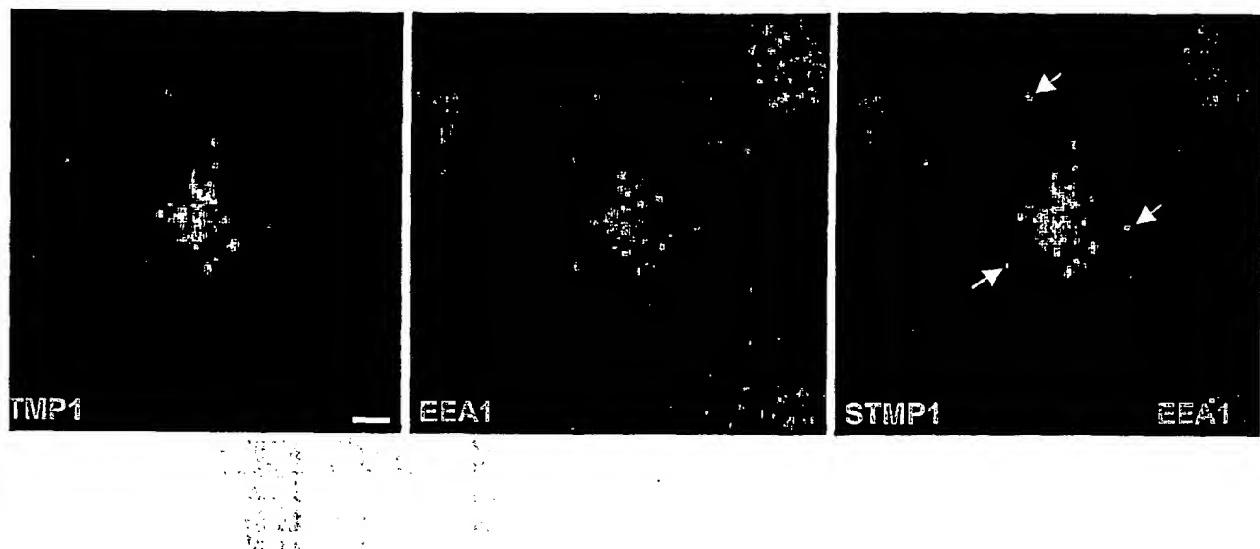


Figure 9

Two mRNA species are transcribed from
the SSH9 gene

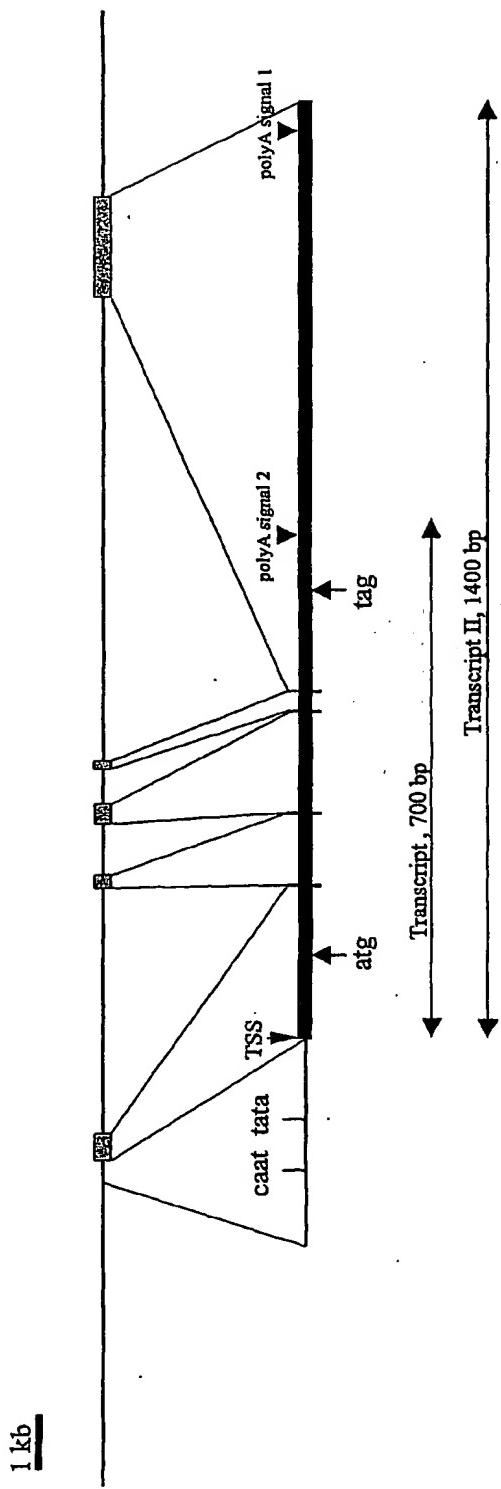


Figure 10

1 AGCGGCGGCTCCTGCAGCGGTGGCTGGCTGTTGGGTGGAGTTTCCCAGCGCCCTCGGG
 1 M T
 62 TCCGACCCCTTGAGCGTTCTGCTCCGGCGCCAGCCTACCTCGCTCCTCGGGCGCCATGACC
 3 T T T T F K G V D P N S R N S S R V L R
 122 ACAACCACCACTTCAGGGAGTCGACCCAAACAGCAGGAATAGCTCCGAGTTTGCGG
 23 P P G G G S N F S L G F D E P T E Q P V
 182 CCTCCAGGTGGTGGATCCAATTTCATTAGGTTTGATGAACCAACAGAACACCTGTG
 43 R K N K M A S N I F G T P E E N Q A S W
 242 AGGAAGAACAAATGGCCTAATATCTTGGGACACCTGAAGAAAATCAAGCTTCTTGG
 63 A K S A G A K S S G G R E D L E S S G L
 302 GCCAAGTCAGCAGGTGCCAAGTCTAGTGGTGGCAGGGAAGACTTGGAGTCATCTGGACTG
 83 Q R R N S S E A S S G D F L D L K G E G
 362 CAGAGAAGGAACCTCTGAAGCAAGCTCCGGAGACTTCTTAGATCTGAAGGGAGAAGGT
 103 D I H E N V D T D L P G S L G Q S E E K
 422 GATATTCATGAAAATGTGGACACAGACTTGGCAGGCCAGGGCAGAGTGAAGAGAAC
 123 P V P A A P V P S P V A P A P V P S R R
 482 CCCGTGCCCTGCTGCGCCTGTGCCAGCCCCGGTGGCCCCGGCCAGTGCCATCCAGAAGA
 143 N P P G G K S S L V L G *
 542 AATCCCCCTGGCGGCAAGTCCAGCCTCGTCTGGTTAGCTCTGACTGTCCCTGAACGCTG
 602 TCGTTCTGTCCTGTTCCCATGCTTGTGAAGTCACAACCTGAGCCTGACTGTACATCT
 662 CTTGGATTTGTTCATTAAAGAAGCACTTTATGTACTGCTGCTTTTTTTTTCTT
 722 TTGAAGAACAGGTTCTCTGTCCTTGACTCTGGGTCTGTGGGCCATGGCATGAGTGT
 782 TTTCTAGTAGAGATTGGAGGGAAAGCTTGTGACACTTAGTACTGTGTTTTAAGAAGA
 842 AATAATTGGTCCAGATGTTAGAGGATCTTTGTACTGAGGTTTTAACACTTACT
 902 TGGGTTTACCAAGCTCAACTGGCACAGACCATAAACAGTCCACAGGCAACGTTCTGCCA
 962 GGCCCCAACCCACAGGGAGCTCTCCGAGAGCCTCTGGTGTGCCCTAACITGCCAG
 1022 TGCCCTTGTCTAGAGCCTCTCTGTGACATGTGAACAATGAAGAGGCCCTGCCCT
 1082 GCCCTGCCCTGCAAAGCAAAGAAACTGCCCTTTATTTTAACCTTAAAGTAGCCA
 1142 GATAGTAACAAGACTGGCTGGCTGATGAGCAAAGCCTTGCTCTCACGCAGAGGAAGGCT
 1202 TGGATGTACAATGAAACTGCCCTGGAACTAAAAGCAGTGAAGCAAGGGAGGCAATCACACT
 1262 GAAGCGGGTCTCCTCCAGGAACGGGGTCCCACAGGCCTGTTGTTAAATAACCTGATG
 1322 CTGTGTGCATGATGCTGGCTTGAACATGAAAGGAAAGTCTCATCCTTAAATGTGTG
 1382 TACTTCACAATCCTGGACTGTTGCTCAAGTAAACATATCCACATTCTAAAAAA
 1442 AAAAAAAAAAAAAAA

FIGURE 11A

FIGURE 11B

Predicted promoter

tgaaaaccc**tataa**aggcgtcgatcgccggacaggcggc**A**gcggcggct

SSH9 EXON-Intron boundaries;

EXON1 CATGACCACAAACcaccac~~tt~~caaggg... INT1 ...tgccattat~~tt~~tcagAGTTTGCGGCCT

EXON2 AAATCAAGCTTCTtggccaagt~~c~~agca... INT2 ...tat~~ttt~~gat~~ttt~~tagGTGCCAAGTCTAG

EXON3 CTAGATCTGAAGgtcagtgt~~g~~acaga... INT4 ...tttttctttctagGGAGAAG

EXON4 GTGATATT~~C~~TGgtaa~~g~~tacttctgaa... INT5 ...tccctgtttcatagAAAATGTGGACAC

FIGURE 11C

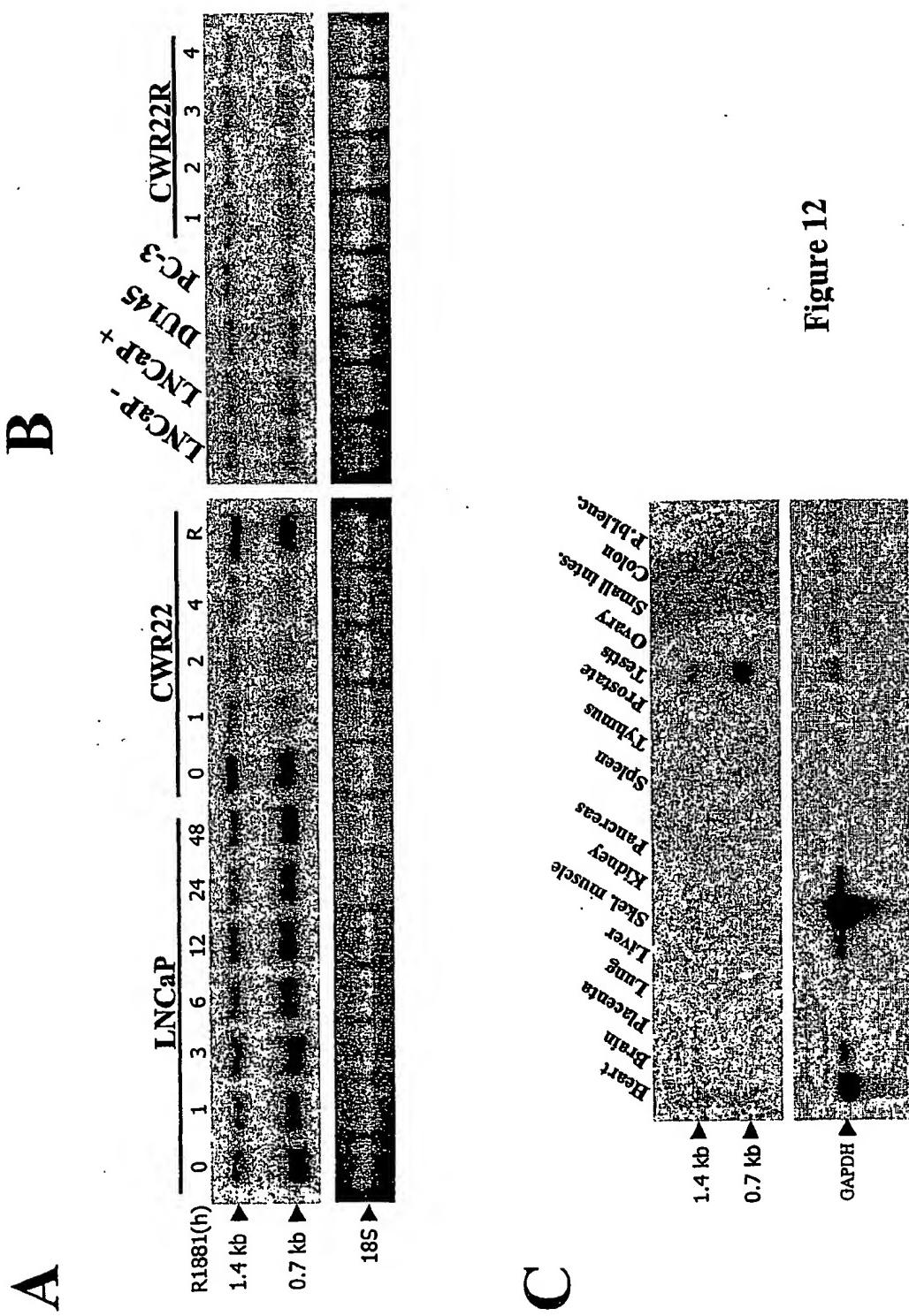


Figure 12

PSL22 gene structure

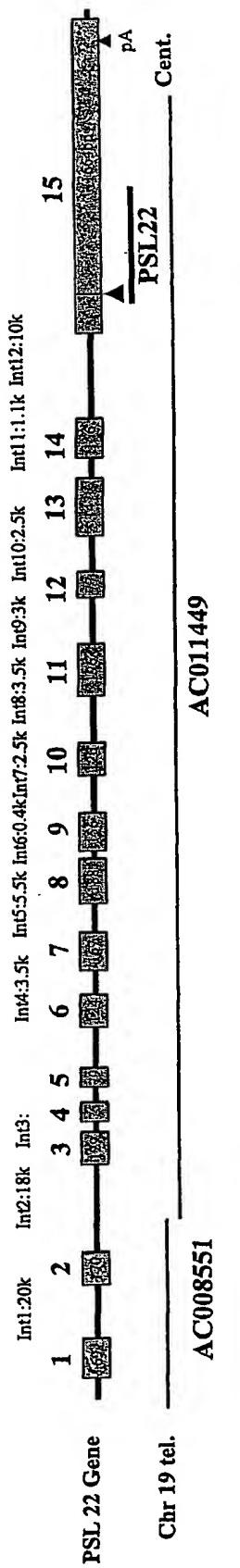


Figure 13

1 ATGACCGACCGCCTGTGCCGCCGGCCCCCAGCCGCTGGAGAAGGAGAACGACGGCTAC
 61 TTTCGGAAGGGCTGTAATCCCCTTGACAAAACCGCCGGAGTAAATTGCAAGAACCAAAGA
 121 GCTGCTTGAATCACAGATCCTGAAAGCGTGCAGGATGAGGACCGGAGCGAAAACCTT
 181 CTGAAAGTGGCCACAAACTCAAAGGTGCGGGAGCAAGTCGGCTGGAGCTGAGCTCGTC
 241 AACTCAGACCTGCAGATGCTCAAGGAAGAGCTGGAGGGCTGAACATCTCGGTGGCGTC
 301 TATCAGAACACAGAGGAGGCATTACGATTCCCTGATTCTCTTGGCCTGAAGGAAACG
 361 AAAGACGTCGACTTGCAGTCGTCCTCAAGGATTATCTGGAACATTACAGTGAAGAT
 421 GGCTATTATATGAAGATGAAATTGCAAGATCTTATGGATCTGAGACAAGCTGTCGGACG
 481 CCTAGCCGGGATGAGGCCGGGGTGAAGTGCAGATGACATACTTCATCCAGCTGGCTTT
 541 GTCGAGAGTCGATTCTTCCGCCACACGGCAGATGGGACTCCTGTTACCTGGTATGAC
 601 TCTCTCACTGGGGTTCGGTCAGCAGCAGAACCTGCTGGAGAAGGCCAGTGTCCCTG
 661 TTCAACACTGGGGCCCTCTACACCCAGATTGGACCCGGTGGCATGGCAGACGCAGGCT
 721 GGGCTGGAGAGTGCATAGATGCCATTTCAGAGAGCCGCAGGGGTTAAATTACCTGAAA
 781 GACACATTACCCATACTCCAAGTTACGACATGAGCCCTGCCATGCTAGCGTGCCTCGTC
 841 AAAATGATGCTTGCACAAGCCAAGAAAGCGTGTGAGAAAATCAGCCTTCTGGATC
 901 CGGAATGAATTCTCATGCTGGTGAAGGTGGCTCAGGAGGCTGCTAAGGTGGAGAGGTC
 961 TACCAACAGCTACACGCAGCCATGAGCCAGGCCAGGGCTGGTAAAGAGAACATCCCCTACTCC
 1021 TGGGCCAGCTTAGCCTGCGTGAAGGCCACCACACGCGCCCTGGCCACTACTTCAC
 1081 GCCATCCTCTCATCGACCAACAGGTGAAGGCCAGCACGGATCTGGACCACCAGGAGAAG
 1141 TGCCCTGCTCCAGCTCTACGACCATGCGAGAGGGCTGACACCCCTGGCCACACTGAAG
 1201 ATGATCAGCAGGCCGACAGCTGGGAAGTCCACTTGGCAGAGCCATGGCTCATCAC
 1261 GAGGAGTCGGTGCAGGCCGAGCCTCTGCAAGAAGCTGGAGCAATTGAGGTGCTACAG
 1321 AAGGTGCTGTTGCGCACAGGAACGCTCCCGCTCACGTACGCCAGCACCAGGAGGAG
 1381 GATGACCTGCTGAACCTGATCGACGCCAGGGCTGACACCCCTGGCCACACTGAAG
 1441 GACATTAATTGCCCAAGTCTCCAGCTGACAGTCACGGACTCTCCAGAAGCTGGGC
 1501 CCCTTATCTGTTTCCGCTAACAGCGGTGGACGCCCTCTGCAAGCATCCGCTTCAC
 1561 GCAGAAGAAGGGGACTTGGGTTCACCTGAGAGGGAACGCCCGGTTCAAGGTTCACTTC
 1621 CTGGATCCTACTGCTCTGCCCGGTGGCAGGAGGCCGGGAGAGGAGATTATATTGCTCC
 1681 ATTGAGCTTGTGGATTGTAAGTGGCTGACGCTGAGTGGTTATGAAGCTGCTGAAGAGC
 1741 TTTGGCGAGGACGAGATCGAGATGAAAGTCGTGAGCCTCTGGACTCCACATCATTG
 1801 CATAATAAGAGTGCACATACTCCGGGAATGCAAGAAAACGTTACTCCATGATCTGCTTA
 1861 GCCATTGATGATGACGACAAAATGATAAAACCAAGAAAATCTCCAAGAAGCTTCCCTTC
 1921 CTGAGTTGGGGCACCAACAAGAACAGACAGAAGTCAGCCAGCACCTGTGCCTCCCATCG
 1981 GTCGGGCTGCACGCCCTCAGGTCAAGAAGAAGCTGCCCTCCCTTCAGCCTCTCAAC
 2041 TCAGACAGTTCTGGTACTAATGTGAGGAAACAAACATGTTCAAGGCCCCGAACATTCCG
 2101 GTGCTGACTCGGCCCTAACGTTGTGCTAACATGAAAATATCTATCTATGCTCTCA
 2161 AATCCTGTTTCTCATAGTGTAAACTCACATTGATGTTTATGAAGGAAAGTAAC
 2221 CAAGAAACCTCTAGGAATTAGTGAAGAAAAGAACCTTTTGAGGTGTGTTACTATACTGCT
 2281 GTAAGTTATTATATTATATAAGTATTGTAATAGAATAGTGTGAAGATAATGAAATATGG
 2341 CTATTTTAATGGTGACAATTATGACTTTAGTCACTATTAAATTGGAAAATATCTATCT
 2401 AGTACAATTGTAGTTGCCAGGTTGGCTAACATCATTCTAACCTAGAACATTAG
 2461 ATGATCCTGAAATTAGGCAGGTCAAGGAGCTGTAATGATAGAACATTAAATTAGTGTCACT
 2521 AAAAATGCTCCAAAGTGTGCTCTCTAACAGAACATTAAACCTAAACAAAGATGTTA
 2581 CTATTATATCGATAGACTATGAATGCTATTCTAGAAAAAGTCTAGTGCCTAACATTGTCT
 2641 TATTAATAAAACAATGTTAGGAGCAGCTTTCTCTAGTTGATGTCATTAAAGAATTA
 2701 CTAACACAGTGGCAGTGTAGATGAAGAGTGTCTAACAGGTAGATAATATACTGTTG
 2761 ATACTCAAACATTTCATTTGTTAAAGTAGAAGATTACATAATTCTATATTAAAGT
 2821 CTTGGGTAAAAAGTAGTTTACATTAAAGTAAAGATGTTAAATGATTAGGTTAA
 2881 AGCTCTATTGACTCCCTTTTGTGAGATAGCGTCTGCTGTGCCCCAGGCTGG
 2941 AGTGCAGTGGTGTGATCTCAGTCAGTCAGCAACCTCCGCCCTGGGATCAAGCGATTCTC
 3001 CTACCTCAGCCTCCCAAATAGCTGGGACTACAAGGTGCCCTCCAGCATGCCCTGGCTGATT
 3061 TTGTTATTTAGTTGAGGTGAGGTTACCATGTTGGCAGGGGGTTCGAAATCCTG
 3121 ACCTCAAATGATCCACCCACCTCAGCCTCCCAAAGTGTGCTGGGATTACAGGCATGCCAC
 3181 CACAACCGTCCCACTATTAACTTTAAAGACATTCTACTGATTGATTATCTT
 3241 GCTATAAGTCGATGACACCGTGAATCTAATAAGGTTCACTGTTGACACAGTACAAGTTA
 3301 CATAGCTAAAATACATAGCATTGAAGAGACTAATTAAAGGATGACAAGAGTTATTTCT
 3361 ATTGTGCAATATCTTAAAGGAAGCAACCACCTTGGGAAAGTGTATCTGCTGCTCTAGG
 3421 GCCATGCTTGATACATATTAAATAACATATTACCTTACCCGAAAAAAAAAAAAAAA
 3481 AAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 14A

1 M T D A L L P A A P Q P L E K E N D G Y
 1 ATGACCGACGCCGTGTTGCCGCCGGCCAGCCGCTGGAGAAGGAGAACGACGGCTAC

 21 F R K G C N P L A Q T G R S K L Q N Q R
 61 TTTCGGAAGGGCTGTAATCCCCTGCAAAACCGGCCGGAGTAAATTGAGAACATCAAAGA

 41 A A L N Q Q I L K A V R M R T G A E N L
 121 GCTGCTTGAAATCAGCAGATCCTGAAAGCCGTGCCGGATGAGGACCGAGCGAAAACCTT

 61 L K V A T N S K V R E Q V R L E L S F V
 181 CTGAAAGTGGCCACAAACTCAAAGGTGCCGGAGCAAGTGCCTGGAGCTGAGCTTCGTC

 81 N S D L Q M L K E E L E G L N I S V G V
 241 AACTCAGACCTGCAGATGCTCAAGGAAGAGCTGGAGGGCTGAACATCTCGGTGGCGTC

 101 Y Q N T E E A F T I P L I P L G L K E T
 301 TATCAGAACACAGAGGAGGCATTACGATTCCCTGATTCCCTTGCGCTGAAGGAAACG

 121 K D V D F A V V L K D F I L E H Y S E D
 361 AAAGACGTCGACTTTGCAGTCGCTCAAGGATTATCCTGGAAACATTACAGTGAAGAT

 141 G Y L Y E D . E I A D L M D L R Q A C R T
 421 GGCTATTTATATGAAGATGAAATTGAGATCTTATGGATCTGAGACAAGCTTGTGGACG

 161 P S R . D E A G V E L L M T Y F I Q L G F
 481 CCTAGCCGGGATGAGGCCGGGTGGAAGTCTGCTGATGACATACTTCATCCAGCTGGCTT

 181 V E S R F F P P T R Q M G L L F T W Y D
 541 GTCGAGAGTCGATTCTCCGCCACACGGCAGATGGACTCCTGTTACCTGGTATGAC

 201 S L T G V P V S Q Q N L L E K A S V L
 601 TCTCTCACTGGGTTCCGGTCAGCCAGAACCTGCTGGAGAAGGCCAGTGTCCCTG

 221 F N T G A L Y T Q I G T R C D R Q T Q A
 661 TTCAACACTGGGCCCTCTACACCCAGATTGGGACCCGGTGCGACAGCAGCAGGCT

 241 G L E S A I D A F Q R A A G V L N Y L K
 721 GGGCTGGAGAGTGCATAGATGCCCTTCAGAGAGCCGAGGGTTAAATTACCTGAAA

 261 D T F T H T P S Y D M S P A M L S V L V
 781 GACACATTACCCATACTCCAAGTTACGACATGAGCCCTGCCATGCTCAGCGTGTGCTC

 281 K M M L A Q A Q E S V F E K I S L P G I
 841 AAAATGATGCTTGCACAAGCCAAGAAAGCGTGTGAGAAAATCAGCCTCCTGGGATC

 301 R N E F F M L V K V A Q E A A K V G E V
 901 CGGAATGAATTCTCATGCTGGTGAAGGTGGCTCAGGAGGCTGCTAAGGTGGAGAGGTC

 321 Y Q Q L H A A M S Q A P V K E N I P Y S
 961 TACCAACAGCTACACGCAGCCATGAGCCAGGCCGGTGAAAGAGAACATCCCCTACTCC

 341 W A S L A C V K A H H Y A A L A H Y F T
 1021 TGGGCCAGCTTAGCCTGCGTGAAGGCCACCACTACGCCGGCCCTGGCCACTACTCACT

 361 A I L L I D H Q V K P G T D L D H Q E K
 1081 GCCATCCTCCTCATCGACCACCAAGGTGAAGGCCAGGCACGGATCTGGACCACCAAGGAGAAG

FIGURE 14B

381 C L S Q L Y D H M P E G L T P L A T L K
 1141 TGCCTGTCAGCTACGACCACATGCCAGAGGGGCTGACACCCCTGGCACACTGAAG

 401 N D Q Q R R Q L G K S H L R R A M A H H
 1201 AATGATCAGCAGCGCCGACAGCTGGGGAGTCCCACTTGCGCAGAGCCATGGCTCATCAC

 421 E E S V R E A S L C K K L R S I E V L Q
 1261 GAGGAGTCGGTGCAGGCGAGCCTTGCAAGAAGCTGCGGAGCATTGAGGTGCTACAG

 441 K V L C A A Q E R S R L T Y A Q H Q E E
 1321 AAGGTGCTGTGCGCACAGGAACGCTCCGGCTACGTACGCCAGCACCAGGAGGAG

 461 D D L L N L I D A P S V V A K T E Q E V
 1381 GATGACCTGCTGAACCTGATCGACGCCAGTGTGCTAAACTGAGCAAGAGGTT

 481 D I I L P Q F S K L T V T D F F Q K L G
 1441 GACATTATATTGCCAGTCTCCAAGCTGACAGTCACGGACTCTTCCAGAAGCTGGC

 501 P L S V F S A N K R W T P P R S I R F T
 1501 CCCTTATCTGTGTTTCGGCTAACAGCGGTGGACGCCCTCGAACATCCGTTCACT

 521 A E E G D L G F T L R G N A P V Q V H F
 1561 GCAGAAGAAGGGACTGGGTTCACCTTGAGAGGGACGCCCGTTAGGTTCACTTC

 541 L D P Y C S A S V A G A R E G D Y I V S
 1621 CTGGATCCTTACTGCTCGCTCGGTGGCAGGAGCCGGAGGAGATTATATTGCTCC

 561 I Q L V D C K W L T L S E V M K L L K S
 1681 ATTGAGCTTGAGATTGTAAGTGGCTGACGCTGAGTGAGGTTATGAAGCTGCTGAAGAGC

 581 F G E D E I E M K V V S L L D S T S S M
 1741 TTTGGCGAGGACGAGATCGAGATGAAAGTCGTGAGCCCTGGACTCCACATCATCCATG

 601 H N K S A T Y S V G M Q K T Y S M I C L
 1801 CATAATAAGAGTGCCACATACTCGTGGAAATGCAGAAAACGTACTCCATGATCTGCTTA

 621 A I D D D D K T D K T K K I S K K L S F
 1861 GCCATTGATGATGACGACAAACTGATAAAACCAAGAAAATCTCCAAGAAGCTTCCATG

 641 L S W G T N K N R Q K S A S T L C L P S
 1921 CTGAGTTGGGGCACCAACAAGAACAGACAGAACAGTCAAGCAGCACCTGTGCCTCCATCG

 661 V G A A R P Q V K K L P S P F S L L N
 1981 GTCGGGGCTGCACGGCCTCAGGTCAAGAAGAAGCTGCCCTCCCTTCAGCCTCTCAAC

 681 S D S S W Y -
 2041 TCAGACAGTTCTGGTACTAATGTGAGGAAACAAACATGTTCAAGGCCCCGAACATTCCG

FIGURE 14B

TATA PROMOTER AND PUTATIVE TRANSCRIPTION START SITE
 AAAAAAAATAAATAAAAGGCCGGCGCGTGGCCCGCCTGCAGCCCC

PSL 22_5'UTR

```

  1 TGCTACTTGGGAGGCTGAGGCTGGAGCATCGCTTGATCCTGGGAGGTGAGGCTGCAAAG
  61 AGTCGAGATCGCAACACTGCTCTCCAGCTGGCGACAGAGCGAGGTCCCCTCTCTTAA
121 AAAAGAACACTGTGCTCAAGGACATCTGCCGTGCTGGGGCGCAAACCCCTCCTGGTCCC
181 CTCTCTCAGGGCAGTCGCGAGCCCAGCGGATCCCCTCGTCTTGCAAGCCGGACAGGG
241 AATCGGCTGAGTTGATCCCCTGCAACAAGCCCGAGTAGTCCGGCAAGGGCCTCGGGG
301 GGCAGTCAACCGCTCCCTCCGCCATGGGCTCCCTCTTGGGAAAGCTTTCAAACCGCC
361 GGGCCCAGGGCCCAGAGCTCCCGCCGCCCTCGACGCTGGCGTCAAGCTGGCCCTTCC
421 CCCGGCGCAGGGCTTCACCCAGGAGGGACGCGGCTGGATCACGCCCTCAGTGA
481 CTCCCCGGGCTTCAGGGCAGGGTGCAGGTCCACAGGCCAGGGCTTCGCTGGGCCCCTGAG
541 ACCCCAGTGCCTTCCCTGCCCTCTCGCCGCACTCGCAAAGTTGAGTCAGGCCACGAGGCC
601 ACAGACAACCCCGAGGGCGCCGCCAGGGCGCAGCTCCGGGTGACGAGCGCCTCAAG
661 GGGCGGGGTTCCGGGCCCGACGGGGCGGGCTCCAGGGCTCCAGTGCCTGGC
721 CTCAGGCAGGGCTAGAAGGGCCGCGGGACGGGGTGGAGTGGAGGGGGGGGGGGGGGG
781 GGACAGGGGGGGGGCGCACGTCCCTCTGGGCCAGGCTCAGGCCCGCCTCAGTCCGC
841 CGTCCGCCCTCCGCGCCCGCGCCCTAGC

```

EXON_1 69bp

```

  1 ATGACCGACGCCGTGTTGCCCGGGCCCCCAGCCGCTGGAGAAGGAGAACGACGGCTAC
  61 TTTCGGAAG

```

EXON_2 117bp

```

  1 GGCTGTAATCCCCCTTGACAAAACCGGCGGAGTAAATTGAGAATCAAAGAGCTGCTT
  61 AATCAGCAGATCCTGAAAGCCGTGCGGATGAGGACCGGAGCGGAAACCTCTGAAA

```

EXON_3 129bp

```

  1 GTGGCCACAAACTCAAAGGTGCGGGACCAAGTGCCTGGAGCTGAGCTTCGTCAA
  61 GACCTGCAGATGCTCAAGGAAGAGCTGGAGGGCTGAACATCTGGTGGCGTATCAG
121 AACACAGAG

```

EXON_4 75bp

```

  1 GAGGCATTACGATTCCCCCTGATTCCCTTGGCTGAAGGAAACGAAAGACGTCGACTTT
  61 GCAGTCGTCCCTCAAG

```

EXON_5 79bp

```

  1 GATTTTATCCTGGAACATTACAGTGAAGATGGCTATTATATGAAGATGAAATTGAGAT
  61 CTTATGGATCTGAGACAAG

```

EXON_6 124bp

```

  1 CTTGCGGACGCCCTAGCCGGATGAGGCCGGGTGGAACCTGCTGATGACATACTTCATCC
  61 AGCTGGCTTGTGAGAGTCGATTCTCCGCCACACGGCAGATGGACTCCTGTTCA
121 CCTG

```

EXON_7 167bp

```

  1 GTATGACTCTCTCACTGGGTTCCGGTCAGCCAGCAGAACCTGCTGGAGAAGGCCAG
  61 TGTCTGTTCAACACTGGGCCCTCTACACCCAGATTGGACCCGGTGCATGGCAGAC
121 GCAGGCTGGCTGGAGAGTGCCTAGATGCCCTTCAGAGAGCCGAG

```

EXON_8 188bp

```

  1 GGGTTTAAATTACCTGAAAGACACATTACCCATACTCCAAGTTACGACATGAGCCCTG
  61 CCATGCTCAGCGTCTCGTAAAATGATGCTTGCACAAGCCAGAAAGCGTGGTGA
121 AAATCAGCCTTCTGGATCCGAATGAATTCTCATGCTGGTGAAGGTGGCTCAGGAGG
181 CTGCTAAG

```

EXON_9 156bp

```

  1 GTGGGAGAGGTCTACCAACAGCTACACCGCAGCCATGAGCCAGGCCAGGGTGAAAGAGAAC

```

FIGURE 14C

61 ATCCCCTACTCCTGGGCCAGCTTAGCCTGCGTGAAGGCCACCACTACGCCGCCTGGCC
 121 CACTACTTCAGGCCATCCTCCTCATCGACCACAG

EXON_10 120bp
 1 GTGAAGCCAGGCACGGATCTGGACCACCAGGAGAAGTGCCTGTCCCAGCTACGACAC
 61 ATGCCAGAGGGCTGACACCCCTGGCCACACTGAAGAATGATCAGCAGGCCGACAGCTG

EXON_11 196bp
 1 GGGAAAGTCCCACCTGCGCAGAGCCATGGCTCATCACGAGGAGTCGGTGCGGGAGGCCAGC
 61 CTCTGCAAGAACGCTCGGGAGCATTGAGGTGCTACAGAAGGTGCTGTGCCCCACAGGAA
 121 CGCTCCCGGCTCACGTACGCCAGCACCAGGAGGATGACCTGCTGAACCTGATCGAC
 181 GCCCCCAGTGTGTTG

EXON_12 77bp
 1 CTTAAACTGAGCAAGAGGTTGACATTATATTGCCCAAGTTCTCCAAGCTGACAGTCACGG
 61 ACTTCTTCCAGAACGCTG

EXON_13 147bp
 1 GGCCCCTTATCTGTGTTTCGGCTAACAGCGGTGGACGCCCTCTCGAACGCATCCGCTTC
 61 ACTGCAGAACAGGGGACTTGGGTTCACCTTGAGAGGGAACGCCCTTCAGGTTCAC
 121 TTCCCTGGATCCTTACTGCTCTGCCCTCG

EXON_14 156bp
 1 GTGGCAGGAGGCCGGAAAGGAGATTATATTGTCTCCATTCAAGCTTGAGGAGATCGAGATG
 61 CTGACGCTGAGTGAGGTTATGAAGCTGCTGAAGAGCTTGGCGAGGACGAGATCGAGATG
 121 AAAGTCGTGAGCCTCCTGGACTCCACATCATCCATG

EXON_15 +3'UTR 1664bp+polyA tract
 1 CATAATAAGAGTGCACACATACTCCGTGGGAATGCAGAAAACGTACTCCATGATCTGCTTA
 61 GCCATTGATGATGACGACAAAACGTATAAAACCAAGAAAATCTCAAGAAGCTTCCCTTC
 121 CTGAGTTGGGGCACCAACAAGAACAGACAGAACAGTCAGCCAGCACCTTGCCCTCC
 181 GTCGGGGCTGACGCCCTCAGGTCAAGAACAGTCAGGCCCTCCCTTGCCCTCAAC
 241 TCAGACAGTTCTGGTACTAATGTGAGGAACAAACATGTTCAAGGCCCGAACATTCCG
 301 GTGCTGACTCGGCCTTAAACGTTGTGCCATAATGGAAAATATCTATCTATCTGTTCTCA
 361 AATCCGTTTCTCATAGTGTAAACTCACATTGATGTGTTTATGAAGGAAAGTAAC
 421 CAAGAACCTCTAGGAATTAGTGAACAAAGAACATTGTTGAGGTGTTACTATACTGCT
 481 GTAAGTTATTATATAAAAGTATTGTAAATAGAATAGTGTGAAGATATGAATATGG
 541 CTATTTTAATGGTACAATTATGACTTTAGTCACTATTAAATTGGGTTACCTATATC
 601 AGTACAATTGTAGTTGTTCCAGGTTGGCTAATAATCATCTTAACTTAGAATTTCAG
 661 ATGATCCTGGAAATTAGGCAGGTCAGAGGACTGTAATGATAATTAAATTAGTGTCACT
 721 AAAACTGTCCAAAGTGTGCTCTCTTAATAGGAATTCAATTAAACCTAAAGATGTTA
 781 CTATTATATCGATAGACTATGAATGCTATTCTAGAAAAGCTAGTGCCTAAATTGTCT
 841 TATTAATAAAACATGTAGGAGCAGCTTCTCTAGTTGATGTCATTAAAGAATTAA
 901 CTAACACAGTGGCAGTGTAGATGAAGATGCTGTCTACAAGGTAGATAATATACTGTTG
 961 ATACTCAAACATTTCATTGTAAAGTAGAAGTTACATAATTCTATATTAAAGT
 1021 CTTGGGTAAAAAAAGTAGTTTACATTAAAGTAAAGATGTAATGATTCAAGGTTAA
 1081 AGCTCTATTGACTTCCTTTTTGTTGAGATAGCGCTTGTGTTGCCAAGGCTGG
 1141 AGTGCAGTGGTGTGATCTCAGCTCAGTGCACCTCCGCCCTGGGATCAAGCGATTCTC
 1201 CTACCTCAGCCTCCAAATAGCTGGACTACAAGGTGCCCTCAGCATGCCCTGGCTGATT
 1261 TTTGTATTGTTAGTTGAGGTGAGGTTTCACCATGTTGGCCAGGCGGGTTTCGAAATCTG
 1321 ACCTCAAATGATCCACCCACCTCAGCCTCCAAAGTGTGCTGGGATTACAGGCATGAGCCAC
 1381 CACAACCGTCCACTATTAACTTTAAAGTACATTCTACTGATTGATTAACTT
 1441 GCTATAAGTCGATGACACCGTGAATCTAATAAGGTTACTGTTGACACAGTACAAGTTA
 1501 CATAGCTAAAATACATAGCATTGAAGACTAATTAAAGGATTGACAAGAGTTATTCT
 1561 ATTGTGCAATATCTTAAAGGAAGCAACCACCTTGGGAAAGTGTATCTGCTCTTAGG
 1621 GCCATGTTGTATACATATTaaataaACATATTCACTTACCCGAAAAAAAAAAAAAA
 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 14C

Rho binding Domain (HR1)

	20	40	60	80	100	120
RhoBD	*	-END-	-END-	-END-	*	*
BBD23615	MTTLLRPPPLPK-----EGDK-----	MTTLLRPPPLPK-----EGDK-----	MTTLLRPPPLPK-----EGDK-----	MTTLLRPPPLPK-----EGDK-----	MTTLLRPPPLPK-----EGDK-----	MTTLLRPPPLPK-----EGDK-----
mBBDph	MILAKLRLGCGEESQQQLS-----	MILAKLRLGCGEESQQQLS-----	MILAKLRLGCGEESQQQLS-----	MILAKLRLGCGEESQQQLS-----	MILAKLRLGCGEESQQQLS-----	MILAKLRLGCGEESQQQLS-----
dRBDph	ADGKELSTAVKNEKKDKEELSCCEK-----	ADGKELSTAVKNEKKDKEELSCCEK-----	ADGKELSTAVKNEKKDKEELSCCEK-----	ADGKELSTAVKNEKKDKEELSCCEK-----	ADGKELSTAVKNEKKDKEELSCCEK-----	ADGKELSTAVKNEKKDKEELSCCEK-----
RhoBP	*	140	160	180	200	220
BBD23615	DLIDIGNEEDVDAVMMVLTENYK-----	DLIDIGNEEDVDAVMMVLTENYK-----	DLIDIGNEEDVDAVMMVLTENYK-----	DLIDIGNEEDVDAVMMVLTENYK-----	DLIDIGNEEDVDAVMMVLTENYK-----	DLIDIGNEEDVDAVMMVLTENYK-----
mBBDph	DLIDIGNEEDVDAVMMVLTENYK-----	DLIDIGNEEDVDAVMMVLTENYK-----	DLIDIGNEEDVDAVMMVLTENYK-----	DLIDIGNEEDVDAVMMVLTENYK-----	DLIDIGNEEDVDAVMMVLTENYK-----	DLIDIGNEEDVDAVMMVLTENYK-----
dRBDph	DLIDIGNEEDVDAVMMVLTENYK-----	DLIDIGNEEDVDAVMMVLTENYK-----	DLIDIGNEEDVDAVMMVLTENYK-----	DLIDIGNEEDVDAVMMVLTENYK-----	DLIDIGNEEDVDAVMMVLTENYK-----	DLIDIGNEEDVDAVMMVLTENYK-----
RhoBP	*	260	280	300	320	340
BBD23615	PRCQDPTQDPTKNSWVQK-----	PRCQDPTQDPTKNSWVQK-----	PRCQDPTQDPTKNSWVQK-----	PRCQDPTQDPTKNSWVQK-----	PRCQDPTQDPTKNSWVQK-----	PRCQDPTQDPTKNSWVQK-----
mBBDph	PRCQDPTQDPTKNSWVQK-----	PRCQDPTQDPTKNSWVQK-----	PRCQDPTQDPTKNSWVQK-----	PRCQDPTQDPTKNSWVQK-----	PRCQDPTQDPTKNSWVQK-----	PRCQDPTQDPTKNSWVQK-----
dRBDph	PRCQDPTQDPTKNSWVQK-----	PRCQDPTQDPTKNSWVQK-----	PRCQDPTQDPTKNSWVQK-----	PRCQDPTQDPTKNSWVQK-----	PRCQDPTQDPTKNSWVQK-----	PRCQDPTQDPTKNSWVQK-----
RhoBP	*	380	400	420	440	460
BBD23615	PDLDIQEKLSQLQNLQK-----	PDLDIQEKLSQLQNLQK-----	PDLDIQEKLSQLQNLQK-----	PDLDIQEKLSQLQNLQK-----	PDLDIQEKLSQLQNLQK-----	PDLDIQEKLSQLQNLQK-----
mBBDph	PDLDIQEKLSQLQNLQK-----	PDLDIQEKLSQLQNLQK-----	PDLDIQEKLSQLQNLQK-----	PDLDIQEKLSQLQNLQK-----	PDLDIQEKLSQLQNLQK-----	PDLDIQEKLSQLQNLQK-----
dRBDph	PDLDIQEKLSQLQNLQK-----	PDLDIQEKLSQLQNLQK-----	PDLDIQEKLSQLQNLQK-----	PDLDIQEKLSQLQNLQK-----	PDLDIQEKLSQLQNLQK-----	PDLDIQEKLSQLQNLQK-----
RhoBP	*	500	520	540	560	580
BBD23615	PDLSKL-----	PDLSKL-----	PDLSKL-----	PDLSKL-----	PDLSKL-----	PDLSKL-----
mBBDph	PDLSKL-----	PDLSKL-----	PDLSKL-----	PDLSKL-----	PDLSKL-----	PDLSKL-----
dRBDph	PDLSKL-----	PDLSKL-----	PDLSKL-----	PDLSKL-----	PDLSKL-----	PDLSKL-----
RhoBD	*	620	640	660	680	700
BBD23615	VEPAPKEDVYVLSQVQV-----	VEPAPKEDVYVLSQVQV-----	VEPAPKEDVYVLSQVQV-----	VEPAPKEDVYVLSQVQV-----	VEPAPKEDVYVLSQVQV-----	VEPAPKEDVYVLSQVQV-----
mBBDph	VEPAPKEDVYVLSQVQV-----	VEPAPKEDVYVLSQVQV-----	VEPAPKEDVYVLSQVQV-----	VEPAPKEDVYVLSQVQV-----	VEPAPKEDVYVLSQVQV-----	VEPAPKEDVYVLSQVQV-----
dRBDph	VEPAPKEDVYVLSQVQV-----	VEPAPKEDVYVLSQVQV-----	VEPAPKEDVYVLSQVQV-----	VEPAPKEDVYVLSQVQV-----	VEPAPKEDVYVLSQVQV-----	VEPAPKEDVYVLSQVQV-----
RhoBP	*	740	760	780	800	820
BBD23615	VKKKDPPESSMSSV-----	VKKKDPPESSMSSV-----	VKKKDPPESSMSSV-----	VKKKDPPESSMSSV-----	VKKKDPPESSMSSV-----	VKKKDPPESSMSSV-----
mBBDph	--H--DPCTNEDVCP-----	--H--DPCTNEDVCP-----	--H--DPCTNEDVCP-----	--H--DPCTNEDVCP-----	--H--DPCTNEDVCP-----	--H--DPCTNEDVCP-----
dRBDph	--SSSEDEPHEPVYAKK-----	--SSSEDEPHEPVYAKK-----	--SSSEDEPHEPVYAKK-----	--SSSEDEPHEPVYAKK-----	--SSSEDEPHEPVYAKK-----	--SSSEDEPHEPVYAKK-----

Figure 15

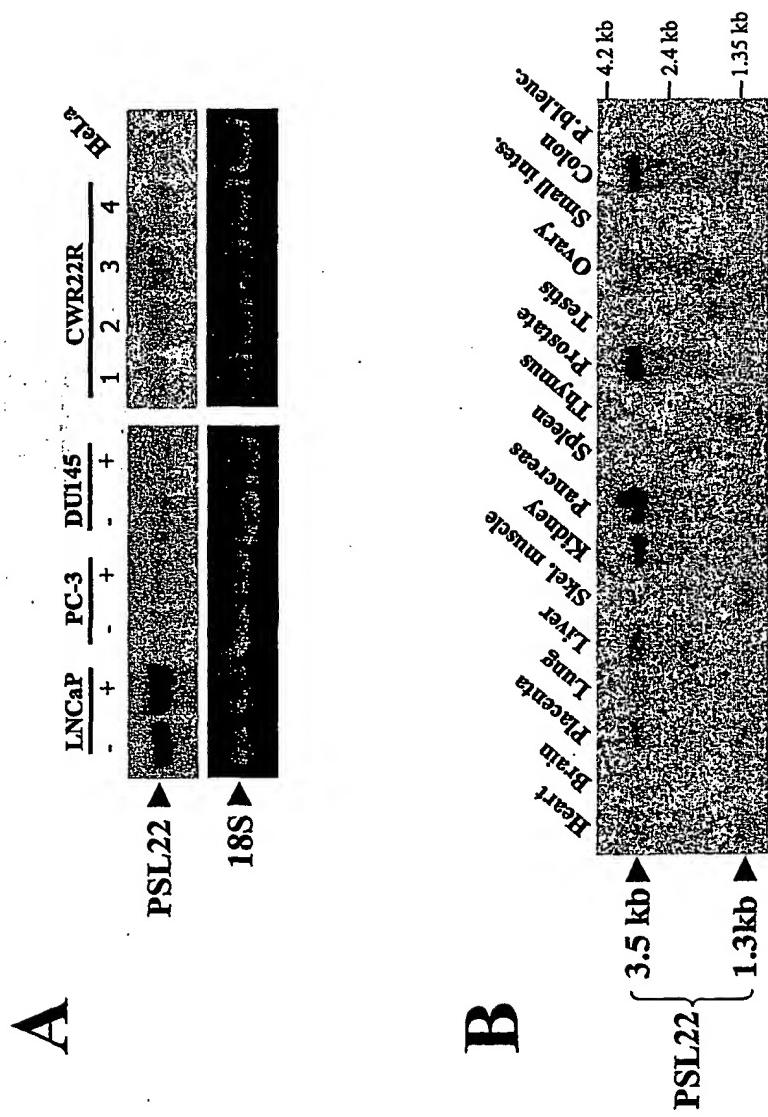


Figure 16

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US01/09410

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C07K 14/00; G01N 33/53; A61K 38/00
US CL : 530/350; 435/7.1; 514/2

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 530/350; 435/7.1; 514/2

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

MPSRCH, DIALOG, WEST

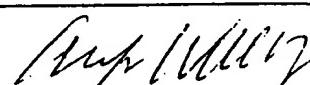
search terms: prostate specific antigen, modulation, expression or activity of prostate specific antigen

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X,P	US 6,048,970 A (LAL et al) 11 April 2000, SEQ ID NO:1 and MPSRCH sequence similarity search report, pages 1-2.	1,7,8
X	US 5,599,686 A (DEFEO-JONES et al) 04 February 1997, claim 12.	19
X	US 5,820,880 A (ALVING et al) 13 October 1998, claim 3.	22

Further documents are listed in the continuation of Box C. See patent family annex.

"	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E"	earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Z"	document member of the same patent family
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search	Date of mailing of the international search report
06 SEPTEMBER 2001	31 OCT 2001
Name and mailing address of the ISA/L'S Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 505-3230	Authorized officer MINH TAM DAVIS  Telephone No. (703) 505-2008

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US01/09410**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1,2,7,8,19,22,SEQ ID NO:14

Remark on Protest

- The additional search fees were accompanied by the applicant's protest.
No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No. PCT/US01/09410

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group 1, claim(s) 1, 2, 7, 8, 19, 22, drawn to a sequence substantially identical to a prostate specific polypeptide of SEQ ID NO:14, and a method for identifying a test compound that modulates the expression or activity of a prostate specific polypeptide.

Groups 2-7, claim(s) 1, 2, 7, 8, 22, drawn to a sequence substantially identical to a prostate specific polypeptide of SEQ ID NO: 29, 32, 34, 36, 41 or 53.

Groups 8-66, claim(s) 3-6, 9-11, 13-16, 25, drawn to nucleic acids of SEQ ID No: 1-12, 15-28, 30, 31, 33, 35, +0, 42-52, 54-70, encoding a prostate specific polypeptide.

Groups 67-124, claim 12, drawn to a transgenic animal comprising the nucleic acid encoding a prostate specific polypeptide.

Groups 125-131, claim 17, drawn to an antibody to a prostate specific polypeptide.

Groups 132-189, claim 18, drawn to a method for detecting a prostate specific gene.

Groups 190-197, claims 20-21, 23-24, drawn to a method of treating a mammal having a disorder of the prostate.

The inventions listed as Groups 1-197 do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

An international stage application shall relate to one invention only or to a group of invention so linked as to form a single general inventive concept. If multiple products, processes of manufacture or uses are claimed, the first invention of the category first mentioned in the claims of the application will be considered as the main invention in the claims, see PCT article 17(3) (a) and 1.476 (c), 37 C.F.R. 1.475(d). Group 1 will be the main invention. After that, all other products and methods will be broken out as separate groups (see 37 CFR 1.475 (d)).

Group 1, drawn to a sequence substantially identical to SEQ ID NO:14 and a method of use of said polypeptide form a single inventive concept.

Groups 2-131 are additional products, which are structurally different from the product of group 1. Further, since a sequence substantially identical to SEQ ID NO:14 is known in the art (MPSRCH sequence similarity search report, pages 1-2, and US patent No: 6,048970), said sequence is not so unique to form a special technical feature.

Groups 132-197 are additional methods which are distinct from the method of group 1 in method's objective, reagents used and method steps.